

| Result No. | Score | Query Match Length DB ID | Description |
|------------|-------|-----------------------------|--|
| 1 | 183 | 100.0 183 19 AA738517 | DNA marker of meta Human UC Band #321 |
| 2 | 183 | 100.0 183 20 AA730719 | DNA encoding novel Human breast cell |
| 3 | 41 | 22.4 2113 23 AA77249 | Human foetal liver Probe #14812 for g Human brain expres |
| 4 | 35.2 | 19.2 164 22 AB51400 | Human bone marrow Probe #14213 for q |
| 5 | 35.2 | 19.2 164 22 AB69411 | AAK79614 DNA encoding novel Human immune/haema |
| 6 | 35.2 | 19.2 164 22 ABA17444 | AAK79614 DNA encoding novel Human immune/haema |
| 7 | 35.2 | 19.2 164 22 AAS91234 | AAK79614 DNA encoding novel Human immune/haema |
| 8 | 35.2 | 19.2 164 22 AAS20261 | AAK79614 DNA encoding novel Human immune/haema |
| 9 | 35.2 | 19.2 164 22 AA738517 | AAK79614 DNA encoding novel Human immune/haema |
| 10 | 33.6 | 18.4 1524 23 ABL30203 | AAK79614 DNA encoding novel Human immune/haema |
| c | 32.8 | 17.9 3819 23 ABL30202 | AAK79614 DNA encoding novel Human immune/haema |
| c | 31.2 | 17.0 3698 22 AAK7760 | AAK79614 DNA encoding novel Human immune/haema |
| c | 31.2 | 17.0 3698 22 AAK83893 | AAK79614 DNA encoding novel Human immune/haema |
| c | 31.2 | 17.0 10548 22 AAK64403 | AAK79614 DNA encoding novel Human immune/haema |
| c | 31.2 | 17.0 10548 22 AAK65913 | AAK79614 DNA encoding novel Human immune/haema |
| c | 31.2 | 17.0 10548 22 AAK73759 | AAK79614 DNA encoding novel Human immune/haema |
| c | 31.2 | 17.0 10548 22 AAKB0611 | AAK79614 DNA encoding novel Human immune/haema |
| c | 30.8 | 17.0 10548 22 AAKB3894 | AAK79614 DNA encoding novel Human immune/haema |
| c | 30.8 | 16.8 5616 22 AAK79614 | AAK79614 DNA encoding novel Human immune/haema |
| c | 30.6 | 16.7 3387 23 AAS91234 | AAK79614 DNA encoding novel Human immune/haema |
| c | 30.6 | 16.7 5216 22 AAS20261 | AAK79614 DNA encoding novel Human immune/haema |
| c | 30.6 | 16.7 5216 22 AAS31528 | AAK79614 DNA encoding novel Human immune/haema |
| c | 30.6 | 16.7 5216 22 ABO6652 | AAK79614 DNA encoding novel Human immune/haema |
| c | 30.2 | 16.5 433 22 AAI89606 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.8 | 16.3 13852 22 ABA17744 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.8 | 16.3 13852 22 ABA17745 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.8 | 16.3 13852 22 ABA21395 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.8 | 16.3 13852 22 ABA21396 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.6 | 16.2 4068 22 AAI86707 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.2 | 16.0 2086 23 ABL12837 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.2 | 16.0 3598 22 AAI64774 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.2 | 16.0 18733 22 AAKB0611 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29.2 | 16.0 100301 24 ABO88176 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29 | 15.8 3212 24 ABK11142 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29 | 15.8 38886 20 AAZ22897 | AAK79614 DNA encoding novel Human immune/haema |
| c | 29 | 15.8 49999 20 AAZ22891 | AAK79614 DNA encoding novel Human immune/haema |
| c | 28.8 | 15.7 431 21 AAC28387 | AAK79614 DNA encoding novel Human immune/haema |
| c | 28.8 | 15.7 1090 18 AAT7290 | AAK79614 DNA encoding novel Human immune/haema |
| c | 28.8 | 15.7 8894 23 ABKA2719 | AAK79614 DNA encoding novel Human immune/haema |
| c | 28.4 | 15.5 1069 24 ABK63447 | AAK79614 DNA encoding novel Human immune/haema |
| c | 41 | 28.4 24 AAS16204 | AAK79614 DNA encoding novel Human immune/haema |
| c | 42 | 28.4 15.5 2513 24 AAS16206 | AAK79614 DNA encoding novel Human immune/haema |
| c | 43 | 28.4 15.5 44576 21 AAZ61522 | AAK79614 DNA encoding novel Human immune/haema |
| c | 44 | 28.2 15.4 341 22 ABA16249 | AAK79614 DNA encoding novel Human immune/haema |
| c | 45 | 28.2 15.4 1907 20 AAV84508 | AAK79614 DNA encoding novel Human immune/haema |

XX Identifying markers for disease states - by amplifying RNA from peripheral blood and identifying RNA which is differential expressed between normal and disease state subjects
PT XX
PT XX
PT XX
PS Claim 17: Page 92; 158pp; English.
XX This sequence represents a DNA marker of metastatic prostate cancer, designated UC Band #321, and was identified using a method of the invention. The method is for identifying markers for a disease state, and comprises: (a) providing a first set of peripheral blood mRNAs from one or more subjects known to exhibit the disease state and a second set of peripheral blood mRNAs from one or more normal subjects; (b) amplifying both sets of mRNAs to provide nucleic acid amplification products; (c) comparing the sets of amplification products; and (d) identifying those mRNAs that are differentially expressed between normal subjects and subjects exhibiting the disease state; where a difference in quantity of expression of an mRNA is indicative of a disease marker. This marker sequence can be used in a method of detecting a metastatic cancer disease state, especially for detection prostate cancer. Using the methods, a disease state may be detected, diagnosed, or a prognosis may be delivered by examining a blood sample rather than relying on a more invasive, or less sensitive test. In addition, a subject may be monitored for disease progression, status and response to therapies through monitoring of differentially expressed disease markers. The methods can be used for diseases such as cancer (especially metastatic or prostate cancer), asthma, lupus erythematosus, rheumatoid arthritis, multiple sclerosis, myasthenia gravis, autoimmune thyroiditis, amyloid lateral sclerosis, interstitial cystitis, prostatitis or other systemic or chronic conditions.

XX Sequence 183 BP; 43 A; 52 C; 45 G; 43 T; 0 other;

Query Match 100.0%; Score 183; DB 19; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.8e-53;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACACACTCCCCCATCTGAGCCAAAGGCCCTACCCPAAGGTGTCAGAGATCAA 60
Db 1 CACACACTCCCCCATCTGAGCCAAAGGCCCTACCCPAAGGTGTCAGAGATCAA 60
Qy 61 GTGCAAGGAGAATGGTAGGCTATTATTCCCAGTGCCTTCCTGGCTAT 120
Db 61 GTGCAAGGAGAATGGTAGGCTATTATTCCCAGTGCCTTCCTGGCTAT 120
Qy 121 GGTGAAACAGTGGCTGACTTCATCTAGGAAGAGCTATGGCTCGTCCTGGCTCA 180
Db 121 GGATGAAACAGTGGCTGACTTCATCTAGGAAGAGCTATGGCTCGTCCTGGCTCA 180
181 CCA 183
Db 181 CCA 183

XX

PN WO9949083-A1.

XX
PD 30-SEP-1999.XX
PP 24-MAR-1999; 99WO-US06488.XX
PR 24-MAR-1998; 98US-0046894.XX
PA (UROC-) UROCOR INC.XX
PI Ralph D, An G, O'Hara SM, Veltri RW;XX
WPI; 1999-591105/50.XX
Identifying markers of human disease, specifically for diagnosis of

PT metastatic prostatic and breast cancers

XX
PS Claim 17; Page 124-125; 225pp; English.XX
This sequence represents a human cDNA sequence designated UC Band #321, which encodes a previously undescribed gene product. The expression of

CC this gene in peripheral leukocytes was examined using reverse

CC transcriptase-PCR (RT-PCR) primers AAZ30739-Z30740. This gene was found

CC to be differentially expressed between healthy subjects and patients

CC with metastatic cancers (especially those of the prostate or breast) and

CC may therefore be used as a marker for such diseases. Detecting

CC levels of such human disease markers is used for diagnosis (also

CC prognosis and monitoring) of diseases, including metastatic or

CC organ-confined cancers, and diseases which also elicit an immune

CC response such as asthma, lupus erythematosus, rheumatoid arthritis,

CC amytrophic lateral sclerosis (ALS), interstitial cystitis and

CC prostatitis, but especially metastatic prostatic and breast cancer. A

CC particular use is differentiating between prostatic and benign

CC prostatic hyper trophy, and between advanced and localised prostatic

CC cancer, by multivariate analysis of several different markers. Cancers

CC can be treated by administering sequences antisense to sequences that

CC encode human disease markers. This method detects a leukocyte response

CC to disease rather than products of diseased cells, so is suitable for

CC large-scale screening of asymptomatic subjects. Disease can be detected

CC at an early stage, when few, if any, diseased cells are present in the

CC circulation. Analysis of blood samples eliminates the need for more

CC invasive methods for obtaining samples.

XX

SQ Sequence 183 BP; 43 A; 52 C; 45 G; 43 T; 0 other;

XX

Query Match 100.0%; Score 183; DB 20; Length 183;

XX

Best Local Similarity 100.0%; Pred. No. 2.8e-53;

XX

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 CACACACTCCCCCATCTGAGCCAAAGGCCCTACCCPAAGGTGTCAGAGATCAA 60

DB 1 CACACACTCCCCCATCTGAGCCAAAGGCCCTACCCPAAGGTGTCAGAGATCAA 60

Qy 61 GTGCAAGGAGAATGGTAGGCTATTATTCCCAGTGCCTTCCTGGCTAT 120

DB 61 GTGCAAGGAGAATGGTAGGCTATTATTCCCAGTGCCTTCCTGGCTAT 120

Qy 121 GGTGAAACAGTGGCTGACTTCATCTAGGAAGAGCTATGGCTCGTCCTGGCTCA 180

DB 121 GGATGAAACAGTGGCTGACTTCATCTAGGAAGAGCTATGGCTCGTCCTGGCTCA 180

181 CCA 183

DB 121 GGATGAAACAGTGGCTGACTTCATCTAGGAAGAGCTATGGCTCGTCCTGGCTCA 180

181 CCA 183

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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.

Homo sapiens.

WO200157275-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00667.

R 04 - FBB-2000; 2000US-0180312.
R 26 - MAY-2000; 2000US-0207456.
R 30 - JUN-2000; 2000US-0608408.
R 03 - AUG-2000; 2000US-0632366.
R 21 - SEP-2000; 2000US-0234687.
R 27 - SEP-2000; 2000US-0236359.
R 04 - OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-483446/52.

Single exon nucleic acid probes for analyzing gene expression in human brains -

Example 4: SEQ ID NO: 17670; 650pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.

| | | | | |
|-----------------------|------------------------|--|------------------|-------|
| XX | PR | 04 -FEB-2000; | 2000US0-0180312. | |
| XX | PR | 26 -MAY-2000; | 2000US0-0207456. | |
| XX | PR | 30 -JUN-2000; | 2000US0-0608048. | |
| XX | PR | 03 -AUG-2000; | 2000US0-0632166. | |
| XX | PR | 21 -SEP-2000; | 2000US0-0234587. | |
| XX | PR | 27 -SEP-2000; | 2000US0-0236359. | |
| XX | PR | 04 -OCT-2000; | 2000US0-0024263. | |
| XX | PA | (MOLE-) MOLECULAR DYNAMICS II | | |
| P1 | Penn SG, | Hanzel DK, | Chen W | |
| XX | DR | WPI; 2001-488900/53. | | |
| XX | PT | Human genome-derived single analyzing gene expression in | | |
| XX | PT | Example 4; SEQ ID NO: 18051; | | |
| XX | PS | The present invention provides probes which are derived from bone marrow. They can be used such as lymphoma, leukaemia samples, which may enable the the probes of the invention. | | |
| CC | CC | CC | | |
| CC | CC | CC | | |
| CC | CC | CC | | |
| CC | CC | CC | | |
| SQ | Sequence | 164 | BP; | 39 A; |
| SQ | Query Match | 19.2% | | |
| | Best Local Similarity | 71.9% | | |
| | Matches | 46; | Conservative | |
| QY | 52 | GAGATCCAAATGCAAGGAGAA | | |
| DB | 100 | | | |
| QY | 112 | CTGGC 115 | | |
| DB | 160 | TGGG 163 | | |
| Query Match | | | | |
| Best Local Similarity | | | | |
| Matches | | | | |
| Matches | | | | |
| Probe: | | | | |
| KW | human; microarray; ge- | | | |
| KW | cervical cancer; ss. | | | |
| XX | Homo sapiens. | | | |
| OS | WO200157378-A2. | | | |
| XX | PN | | | |
| XX | PD | 09 -AUG-2001. | | |
| XX | PF | 30 -JAN-2001; | 2001WO-US000670. | |
| XX | PR | 04 -FEB-2000; | 2000US0-0180312. | |
| PR | 26 -MAY-2000; | 2000US0-0207456. | | |
| PR | 30 -JUN-2000; | 2000US0-0608048. | | |
| PR | 03 -AUG-2000; | 2000US0-0632166. | | |
| PR | 21 -SEP-2000; | 2000US0-0234587. | | |
| PR | 27 -SEP-2000; | 2000US0-0236359. | | |
| PR | 04 -OCT-2000; | 2000US0-0024263. | | |
| XX | PA | (MOLE-) MOLECULAR DYNAMICS II | | |

Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
 PS Claim 25; SEQ ID No 14213; 487BP; English.
 The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.
 Sequence 164 BP; 39 A; 39 C; 44 G; 42 T; 0 other;
 Query Match Score 19.28; Best Local Similarity 71.98; Pred. No. 0.031; Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 Qy 52 GAGATCCAAAGTGAGGAGAATGGTGGAGCTATTATCCTCCCGATGTGCCCTCCGT 11
 Db 100 GAGATCAGAGCAGAAAGAGATGAAGTGGAGATTTATTCCTGGCTCTCTCTG 159
 Qy 112 CTGG 115
 Db 160 TGGG 163
 RESULT 10
 ABL30203 ID ABL30203 standard; DNA; 1524 BP.
 XX AC ABL30203;
 XX DT 26-MAR-2002 (first entry)
 Drosophila melanogaster genomic polynucleotide SEQ ID NO 42082.
 XX DE Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ds.
 XX OS Drosophila melanogaster.
 XX PN WO2001171042-A2.
 XX PR 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 XX Claim 1; SEQ ID NO 42082; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 XX Claim 1; SEQ ID NO 42082; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is capable of detecting 1000 or more genes from Drosophila. The invention is

CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct.html](http://wipo.int/pub/published_pct.html).

| | | |
|----|--|---------------------------------|
| CC | Sequence 3819 BP; 1093 A; 806 C; 787 G; 1133 T; 0 other; | PR 22-AUG-2000; 2000US-0227182. |
| CC | Best Local Similarity 55.2%; Pred. No. 0.74; | PR 23-AUG-2000; 2000US-0227009. |
| XX | Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0; | PR 30-AUG-2000; 2000US-022824. |
| SQ | Query Match 17.9%; Score 32.8; DB 23; Length 3819; | PR 01-SEP-2000; 2000US-0229387. |
| | | PR 01-SEP-2000; 2000US-0229343. |
| | | PR 01-SEP-2000; 2000US-0229344. |
| | | PR 05-SEP-2000; 2000US-0229345. |
| | | PR 05-SEP-2000; 2000US-0229309. |
| | | PR 05-SEP-2000; 2000US-0229513. |
| | | PR 06-SEP-2000; 2000US-0230437. |
| | | PR 06-SEP-2000; 2000US-0230438. |
| | | PR 08-SEP-2000; 2000US-0231242. |
| | | PR 08-SEP-2000; 2000US-0231243. |
| | | PR 08-SEP-2000; 2000US-0231244. |
| | | PR 08-SEP-2000; 2000US-0231245. |
| | | PR 12-SEP-2000; 2000US-0231246. |
| | | PR 08-SEP-2000; 2000US-0232080. |
| | | PR 08-SEP-2000; 2000US-0232081. |
| D | RESULT 12 | PR 14-SEP-2000; 2000US-0232397. |
| D | AAK73760 standard; DNA; 3698 BP. | PR 14-SEP-2000; 2000US-0232399. |
| XX | AAK73760; | PR 14-SEP-2000; 2000US-0232400. |
| AC | | PR 14-SEP-2000; 2000US-0232401. |
| XX | DT 07-NOV-2001 (first entry) | PR 14-SEP-2000; 2000US-0233063. |
| XX | | PR 14-SEP-2000; 2000US-0233064. |
| XX | | PR 14-SEP-2000; 2000US-0233065. |
| DE | Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28572. | PR 21-SEP-2000; 2000US-0234223. |
| XX | KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; | PR 21-SEP-2000; 2000US-0234240. |
| KW | cytostatic; gene therapy; vaccine; metastasis; ds. | PR 25-SEP-2000; 2000US-0234397. |
| XX | | PR 26-SEP-2000; 2000US-0234398. |
| OS | Homo sapiens. | PR 27-SEP-2000; 2000US-0235894. |
| XX | XX | PR 27-SEP-2000; 2000US-0235836. |
| NN | WO200157182-A2. | PR 29-SEP-2000; 2000US-0236327. |
| XX | XX | PR 29-SEP-2000; 2000US-0236367. |
| PD | 09-AUG-2001. | PR 29-SEP-2000; 2000US-0236368. |
| XX | PF 17-JAN-2001; 2001WO-US01354. | PR 29-SEP-2000; 2000US-0236369. |
| XX | XX | PR 29-SEP-2000; 2000US-0236370. |
| PR | 31-JAN-2000; 2000US-0179065. | PR 02-OCT-2000; 2000US-0236602. |
| PR | 04-FEB-2000; 2000US-0180628. | PR 02-OCT-2000; 2000US-0237037. |
| PR | 24-FEB-2000; 2000US-0184664. | PR 02-OCT-0000; 2000US-0237038. |
| PR | 02-MAR-2000; 2000US-0186350. | PR 02-OCT-2000; 2000US-0237039. |
| PR | 16-MAR-2000; 2000US-0188874. | PR 13-OCT-2000; 2000US-0239935. |
| PR | 17-MAR-2000; 2000US-019076. | PR 13-OCT-2000; 2000US-0239937. |
| PR | 18-APR-2000; 2000US-0198123. | PR 20-OCT-2000; 2000US-0240960. |
| PR | 19-MAY-2000; 2000US-0205515. | PR 20-OCT-2000; 2000US-0241221. |
| PR | 07-JUN-2000; 2000US-0209467. | PR 20-OCT-2000; 2000US-0241785. |
| PR | 28-JUN-2000; 2000US-0214886. | PR 20-OCT-2000; 2000US-0241786. |
| PR | 30-JUN-2000; 2000US-0215135. | PR 20-OCT-2000; 2000US-0241787. |
| PR | 07-JUL-2000; 2000US-021647. | PR 20-OCT-2000; 2000US-0241808. |
| PR | 07-JUL-2000; 2000US-0216880. | PR 20-OCT-2000; 2000US-0241809. |
| PR | 11-JUL-2000; 2000US-0217487. | PR 01-NOV-2000; 2000US-0241826. |
| PR | 14-JUL-2000; 2000US-0217496. | PR 08-NOV-2000; 2000US-0244617. |
| PR | 14-AUG-2000; 2000US-0218290. | PR 08-NOV-2000; 2000US-024674. |
| PR | 14-AUG-2000; 2000US-0220963. | PR 08-NOV-2000; 2000US-0246475. |
| PR | 26-JUL-2000; 2000US-0220964. | PR 08-NOV-2000; 2000US-0246476. |
| PR | 14-AUG-2000; 2000US-0224518. | PR 08-NOV-2000; 2000US-0246527. |
| PR | 14-AUG-2000; 2000US-0224519. | PR 08-NOV-2000; 2000US-0246528. |
| PR | 14-AUG-2000; 2000US-0225170. | PR 08-NOV-2000; 2000US-0246529. |
| PR | 14-AUG-2000; 2000US-0225113. | PR 08-NOV-2000; 2000US-0246530. |
| PR | 14-AUG-2000; 2000US-0225214. | PR 08-NOV-2000; 2000US-0246531. |
| PR | 14-AUG-2000; 2000US-0225157. | PR 08-NOV-2000; 2000US-0246532. |
| PR | 14-AUG-2000; 2000US-0225158. | PR 08-NOV-2000; 2000US-0246535. |
| PR | 14-AUG-2000; 2000US-0225159. | PR 08-NOV-2000; 2000US-0246611. |
| PR | 18-AUG-2000; 2000US-0226279. | PR 08-NOV-2000; 2000US-0246613. |
| PR | 22-AUG-2000; 2000US-0226681. | PR 17-NOV-2000; 2000US-0249207. |
| PR | 22-AUG-2000; 2000US-0226688. | PR 17-NOV-2000; 2000US-0249208. |

| Db | 650 CAAAGTCATTCTAAAGAACCTAAATGCCGTTGGTGGCTCAC 69 |
|-----------------------|--|
| PR | 17 -NOV-2000; 2000US-0249209. |
| PR | 17 -NOV-2000; 2000US-0249110. |
| PR | 17 -NOV-2000; 2000US-0249111. |
| PR | 17 -NOV-2000; 2000US-0249212. |
| PR | 17 -NOV-2000; 2000US-0249114. |
| PR | 17 -NOV-2000; 2000US-0249215. |
| PR | 17 -NOV-2000; 2000US-0249116. |
| PR | 17 -NOV-2000; 2000US-0249217. |
| PR | 17 -NOV-2000; 2000US-0249118. |
| PR | 17 -NOV-2000; 2000US-0249244. |
| PR | 17 -NOV-2000; 2000US-0249245. |
| PR | 17 -NOV-2000; 2000US-0249264. |
| PR | 17 -NOV-2000; 2000US-0249265. |
| PR | 17 -NOV-2000; 2000US-0249297. |
| PR | 17 -NOV-2000; 2000US-0249299. |
| PR | 17 -NOV-2000; 2000US-0249300. |
| PR | 01 -DEC-2000; 2000US-0250160. |
| PR | 01 -DEC-2000; 2000US-0250191. |
| PR | 05 -DEC-2000; 2000US-0251030. |
| PR | 05 -DEC-2000; 2000US-0251988. |
| PR | 05 -DEC-2000; 2000US-0256719. |
| PR | 08 -DEC-2000; 2000US-0251179. |
| PR | 08 -DEC-2000; 2000US-0251856. |
| PR | 08 -DEC-2000; 2000US-0251868. |
| PR | 08 -DEC-2000; 2000US-0251869. |
| PR | 08 -DEC-2000; 2000US-0251989. |
| PR | 08 -DEC-2000; 2000US-0251990. |
| PR | 11 -DEC-2000; 2000US-0251997. |
| PR | 05 -JAN-2001; 2001US-0259678. |
| XX | (HUMA-) HUMAN GENOME SCI INC. |
| PA | XX |
| PI | Rosen CA, Barash SC, Ruben SM; |
| XX | WPI: 2001-483426/52. |
| PT | Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. |
| PT | Disclosure; SEQ ID NO 28572; 3071PP + Sequence Listing; English. |
| CC | AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AM82170 to AM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with increased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK51950 and AAM82169 represent sequences used in the exemplification of the present invention. |
| SQ | Sequence 3698 BP; 1067 A; 884 C; 788 G; 959 T; 0 other; |
| Query Match | 17.0% |
| Best Local Similarity | 55.6% |
| Matches 60; | Conservative 0; Mismatches .48; Indels 0; Gaps 0; |
| PR | 01 -SEP-2000; 2000US-0229343. |
| PR | 01 -SEP-2000; 2000US-0229344. |
| PR | 01 -SEP-2000; 2000US-0229345. |
| PR | 05 -SEP-2000; 2000US-0229509. |
| PR | 06 -SEP-2000; 2000US-0229513. |
| PR | 06 -SEP-2000; 2000US-0231242. |
| PR | 08 -SEP-2000; 2000US-0231243. |
| PR | 08 -SEP-2000; 2000US-0231244. |
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XX PI Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-483426/52.

XX PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

XX PS Disclosure; SEQ ID NO 19515; 3071pp + Sequence Listing; English.

XX CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM81921 to AAM81920. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK6703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 10548 BP; 3143 A; 2302 C; 2158 G; 2945 T; 0 other;

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 PR 14-SEP-2000; 2000US-0233354.
 PR 14-SEP-2000; 20

| Result | No. | Query | Score | Match | Length | DB | ID | Description |
|--|---|---|-------|-------|--------|------|----------|----------------------|
| c 1 | 41.2 | BG161919 dc43b12_y | 7 | 34 | 18.6 | 283 | 12 | BG161919 |
| | | AI51580 LD44491.5 | c 9 | 33 | 18.4 | 695 | 9 | AI51280 |
| | | AI24308 qh41b03.x | c 10 | 33 | 18.0 | 438 | 9 | AI24308 |
| | | AI80410 wf27f08.x | c 11 | 33 | 18.0 | 467 | 9 | AI80610 |
| OM nucleic - nucleic search, using sw model | | BH274856 CH230-48J | c 12 | 33 | 18.0 | 481 | 17 | BH274856 |
| Run on: | May 25, 2003, 03:09:12 ; Search time 1754 Seconds (without alignments) | BH268816 BM663839 UI-E-CLL- | c 13 | 32.8 | 17.9 | 594 | 17 | BH268816 |
| | 1689.723 Million cell updates/sec | AL107572 Drosophila | c 14 | 32.8 | 17.9 | 582 | 13 | BM663839 |
| | | AQ543989 RPCI-11-3 | c 15 | 32.4 | 17.7 | 994 | 17 | CNS074A |
| Title: | US-09-660-568-49 | B01998 CSRL-145D12 | c 16 | 32.4 | 17.7 | 226 | 17 | AQ543989 |
| Perfect score: | 183 | AQ09155 HS-5323_B | c 17 | 32.4 | 17.7 | 524 | 17 | AQ09155 |
| Sequence: | 1 cacacactcccccattctga.....ctgtctcggaggactcca 183 | BG72090 6026910-09 | c 18 | 32.4 | 17.7 | 609 | 12 | BG72090 |
| Scoring table: | IDENTITY_NUC | AZ745700 RPCI-24-1 | c 19 | 32 | 17.5 | 365 | 17 | AZ745700 |
| Gapop 10.0 , Gapext 1.0 | 20 | BH307258 CH230-10L | c 20 | 32 | 17.5 | 401 | 17 | BH307258 |
| Searched: | 16154066 seqs, 8097743376 residues | H32274 EST10704 R | c 21 | 31.8 | 17.4 | 455 | 17 | AQ536443 RPCI-11-3 |
| Total number of hits satisfying chosen parameters: | 32308132 | BG605222 WHE2662_B | c 22 | 31.8 | 17.4 | 591 | 12 | BG605222 |
| Minimum DB seq length: 0 | 28 | BE10967 384147_MA | c 23 | 31.6 | 17.3 | 638 | 17 | BE10967 |
| Maximum DB seq length: 2000000000 | 29 | BE082216 QV2-BT063 | c 24 | 31.6 | 17.3 | 638 | 17 | BE082216 |
| Post-processing: Minimum Match 0% | 30 | AL510875 AL510875 | c 25 | 31.6 | 17.3 | 649 | 13 | AL510875 |
| Post-processing: Maximum Match 100% | 31 | BH361239 CH230-6C | c 26 | 31.4 | 17.2 | 258 | 14 | BH361239 |
| Listing first 45 summaries | c 27 | H32274 EST10704 R | c 28 | 31.4 | 17.2 | 308 | 17 | AQ252041 HS_3024_B |
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| | 2: em_estbm:* | BE082216 QV2-BT063 | c 31 | 31.4 | 17.2 | 634 | 9 | BE082216 |
| | 3: em_estin:* | AL510875 AL510875 | c 32 | 31.2 | 17.0 | 316 | 17 | AL510875 |
| | 4: em_estmu:* | BH361239 CH230-6C | c 33 | 31.2 | 17.0 | 446 | 17 | BH361239 |
| | 5: em_estov:* | AQ536443 RPCI-11-4 | c 34 | 31.2 | 17.0 | 524 | 17 | AQ536443 |
| | 6: em_estp1:* | AQ977475 RPCI-23-3 | c 35 | 31.2 | 17.0 | 623 | 10 | AQ977475 |
| | 7: em_estro:* | AQ177467 HS_2203_B | c 36 | 31.2 | 17.0 | 535 | 17 | AQ177467 |
| | 8: em_htc:* | AQ284523 RPCI11-77 | c 37 | 31 | 16.9 | 502 | 17 | AQ284523 |
| | 9: qb_est1:* | AZ633721 IM0488C11 | c 38 | 31 | 16.9 | 502 | 17 | AZ633721 |
| | 10: qb_est2:* | AZ217607 Sheared_D | c 39 | 31 | 16.9 | 1082 | 17 | AZ217607 |
| | 11: qb_htc:* | AZ792647 2M0045F14 | c 40 | 30.8 | 16.8 | 524 | 17 | AZ792647 |
| | 12: qb_est3:* | AL43513 T3 end of | c 41 | 30.8 | 16.8 | 425 | 17 | AL43513 |
| | 13: qb_est4:* | CGN078V | c 42 | 30.8 | 16.8 | 481 | 17 | CGN078V |
| | 14: qb_est5:* | BG190341 RST904_A | c 43 | 30.8 | 16.8 | 514 | 17 | BH288367 |
| | 15: em_estfun:* | BH860338 UP_294-17 | c 44 | 30.8 | 16.8 | 517 | 14 | BH860338 |
| | 16: em_gss:* | AQ732988 HS_5104_A | c 45 | 30.8 | 16.8 | 577 | 17 | AQ732988 |
| | 17: em_gss_hum:* | BQ090484 rc66503_Y | | | | | | BQ090484 |
| | 18: em_gss_inv:* | AQ189764 HS_3224_A | | | | | | AQ189764 |
| | 19: em_gss_pbn:* | | | | | | | |
| | 20: em_gss_vrt:* | | | | | | | |
| | 21: em_gss_fun:* | | | | | | | |
| | 22: em_gss_mam:* | | | | | | | |
| | 23: em_gss_mus:* | | | | | | | |
| | 24: em_gss_pro:* | | | | | | | |
| | 25: em_gss_other:* | | | | | | | |
| | 26: em_gss_rod:* | | | | | | | |
| | 27: em_gss_ron:* | | | | | | | |
| | RESULT 1 | | | | | | | |
| | BG775699/c | BG775699 961 bp mRNA | | | | | | |
| | LOCUS | 6026500701 NIH_MGC_40 Homo sapiens | | | | | | |
| | DEFINITION | mRNA clone IMAGE:4760993 3 , | | | | | | |
| | | mRNA sequence. | | | | | | |
| | ACCESSION | BG775699 | | | | | | |
| | VERSION | BG775699.1 | | | | | | |
| | KEYWORDS | GI:14046016 | | | | | | |
| | SOURCE | EST. | | | | | | |
| | ORGANISM | Homo sapiens | | | | | | |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | |
| | | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | | | | |
| | REFERENCE | NIH-MGC http://mgc.ncbi.nlm.nih.gov/ | | | | | | |
| | AUTHORS | 1 (bases 1 to 961) | | | | | | |
| | TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | | | |
| | JOURNAL | Unpublished (1999) | | | | | | |
| | COMMENT | Contact: Robert Straussberg, Ph.D. | | | | | | |
| | | Email: cgapbs-r@mail.nih.gov | | | | | | |
| | | Tissue Procurement: DCTD/DTP | | | | | | |
| | | CDNA Library Preparation: Ling Hong/Rubin Laboratory | | | | | | |
| | | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) | | | | | | |
| | | DNA Sequencing by: Incyte Genomics, Inc. | | | | | | |
| | | Clone distribution: MGCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: | | | | | | |
| | | http://image.llnl.gov | | | | | | |
| | | Plate: LLCM1612 row: 1 column: 18 | | | | | | |
| | | High quality sequence start: 4 | | | | | | |
| | | High quality sequence stop: 783. | | | | | | |
| | | Location/Qualifiers | | | | | | |
| | SUMMARIES | | | | | | | |
| | Result No. | Query | Score | Match | Length | DB | ID | Description |
| | c 1 | BG161919 dc43b12_y | 41.2 | 22.5 | 961 | 12 | BG775699 | BG775699 961 bp mRNA |
| | c 2 | AI51580 LD44491.5 | 37.6 | 20.5 | 501 | 17 | BH309749 | AI51280 |
| | c 3 | AI24308 qh41b03.x | 37 | 20.2 | 506 | 17 | AQ19671 | AI24308 |
| | c 4 | AI80410 wf27f08.x | 36.6 | 20.0 | 789 | 17 | BH274856 | AI80410 |
| | c 5 | BH274856 CH230-48J | 35.4 | 19.3 | 702 | 12 | BH317352 | BH274856 |
| | c 6 | BH317352 CH230-119 | 34.2 | 18.7 | 831 | 12 | BG719810 | BH317352 |
| | | BG719810 602691217 | | | | | | |
| | | BF571585 602078004 | | | | | | |
| | FEATURES | | | | | | | |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

source 1. .961
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:476093"
 /clone_lib="NTH_MGC_40"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage resistant)"
 /note="Organ: prostate; Vector: pMB7; Site_1: XbaI;
 Directionally cloned into EcoRI/XbaI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and SuperScript II RT (Life Technologies).
 Note: this is a NIH MGC Library."
 BASE COUNT 211 a 268 c 252 g 230 t
 ORIGIN

Query Match 22.5%; Score 41.2; DB 12; Length 961;
 Best Local Similarity 56.7%; Pred. No. 0.057;
 Matches 76; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 Qy 9 CCCCCATTCTGACCCCAAGAGGCTATCCCTTAAGGATGCCAGATCCAACTGCCAGAA 68
 Db 960 CCCACCTCTGGTTCCACCTGGCTCATCCCCACACAACCGATGATGCCAGAATGAA 901

Qy 69 GGAAATGTGGTGAAGCTTATTATCCCCCAGTCCTGCTGGCTATGGTGAAC 128
 Db 900 GGCGATTCGGCTGGCTGTGATGTTACTGAAGACGGCACTTTGGTGCCGAAACGAGTGAC 841

Qy 129 ATGGCTGACTTCA 142
 Db 840 ATGGCAGACTCA 827

RESULT 2 BH309749 501 bp DNA linear GSS 03-DEC-2001
 LOCUS CH230-181E7.TU CHORI-230 Segment 1 Rattus norvegicus genomic clone
 DEFINITION CH230-181E7, DNA sequence.
 ACCESSION BH309749
 VERSION BH309749.1 GI:17235218
 SOURCE GSS.
 ORGANISM Rattus norvegicus
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Rattus.
 AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsengayev,G., Geer,K., Shvartsbeyn
 A., Gebregiorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
 Jong,P. and Fraser,C.M.
 TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: zhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/>). For BAC library
 availability, please contact Pieter de Jong (pdeJong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/>) or ering-information.htm). BAC end
 page: http://www.tigr.org/tigrdb/bac_ends/rat/pac_end_intro.html
 Plate: 181 row: E column: 7
 Seq primer: SP6
 Class: BAC ends.
 FEATURES source
 1. .501

source 1. .506
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 /db_xref="GDB:7568307"
 /clone="CH230-181E7"
 /clone.lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: PIARBA2.1; Site_1: EcoRI; Site_2: EcoRI;
 CHORI-230 Rat (BN/SSNNHsd/MCW) BAC library produced by
 Pieter de Jong."
 BASE COUNT 136 a 150 c 135 g 80 t
 ORIGIN

Query Match 20.5%; Score 37.6; DB 17; Length 501;
 Best Local Similarity 63.0%; Pred. No. 0.53;
 Matches 58; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Qy 88 TTATTCCCCAGTGCCTTCCTGCTGGCTATGGTACAGTGGCTACTCTCATCTAG 147
 Db 114 TTTCGCTGAAAGTGTGACCTGCTGTGAACTCTGACACAGGGCAATTCCTCTAG 173

Qy 148 GAAAGAGCTATGGCTCTGCTCTGCTCTGGAGCT 179
 Db 174 GACCGGCACTTCCGTGTTACCGAGGCC 205

RESULT 3 AQ419671
 LOCUS AQ419671
 DEFINITION RPCI-11-179B12.TU RPCI-11 Homo sapiens genomic clone RPCI-11-179B12
 ACCESSION AQ419671
 VERSION AQ419671.1 GI:4477395
 SOURCE GSS.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 ZHAO,S., Adams,M.D., Niernan,W., Malek,J., de Jong, P. and Venter
 ,J.C.,
 REFERENCE AUTHORS
 TITLE use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 JOURNAL MAP Building
 COMMENT Unpublished (1997)
 Other GSS: RPCI-11-179B12.TU
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (Pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tigrdb/humgen/bac_end_search.html.
 Seq primer: SP6
 Class: BAC ends.
 FEATURES Location/Qualifiers
 1. .506

source 1. .506
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 /db_xref="GDB:7568307"
 /clone="RPCI-11-179B12"
 /clone.lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: PBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 BASE COUNT 106 a 121 c 110 g 169 t
 ORIGIN

| | | | | | | | |
|--------------------------|---|--|--------------------|-------------------------------------|--|---|----------------|
| Query Match | 20.2% | Score 37; | DB 17; | Length 506; | Qy | 145 TAGGAAGAGCTATGGCTTGTGTCAGTCACCA 183 | |
| Best Local Similarity | 71.0% | Pred. No. | 0.81; | | Db | 585 TAGGCCGGCATTCCTGGTACGGAGTCACCA 547 | |
| Matches 49; conservative | 0; | Mismatches | 20; | Indels | 0; | Gaps | 0; |
| | | | | | | | |
| Qy | 89 TTATTCCCCAAGTGCCTTCTGTGGCTATGGATGAACTGCGTGCATCTAGG 148 | | | | RESULT 5 | | |
| Db | 321 TTATTCCCCAAGTGCCTTCTGTGGCTATGGATGAACTGCGTGCATCTAGG 148 | | | | BG719810/0/C | BG719810 | 702 bp mRNA |
| | | | | | LOCUS | 602691217F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823333 5' , | |
| Qy | 149 AAAGAGCTA 157 | | | | DEFINITION | | |
| Db | 381 GAAGATGTA 389 | | | | ACCESSION | BG719810 | |
| | | | | | VERSION | BG719810.1 | EST |
| | | | | | KEYWORDS | GI:13998997 | |
| | | | | | SOURCE | | |
| | | | | | ORGANISM | Homo sapiens | |
| | | | | | Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | | | | | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | |
| LOCUS | BH317352 | CH310-119L10 TVB CHORI-230 | 789 bp | DNA linear | REFERENCE | 1 (bases 1 to 702) | |
| DEFINITION | | clone CH310-119L10, | | Segment 1 Rattus norvegicus genomic | NM-MGC | http://mgc.ncbi.nih.gov/ | |
| ACCESSION | BH317352 | | | | TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | |
| VERSION | BH317352.1 | GI:17248066 | | | JOURNAL | Unpublished (1999), | |
| SOURCE | | Rattus norvegicus | | | COMMENT | Contact: Robert Strausberg, Ph.D. | |
| ORGANISM | | Mammalia; Eutheria; Rodentia; Murinae; | | | Email: cgabps@mail.nih.gov | | |
| | | Chordata; Craniata; Vertebrata; Euteleostomi; | | | Tissue Procurement: Miklos Palkovits, M.D., Ph.D. | | |
| | | Sciurognathi; Muridae; | | | cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki | | |
| | | Shvartsbeyn, Toshiyuki and Piero Carninci (RIKEN) | | | DNA Sequencing by: Incyte Genomics, Inc. | | |
| REFERENCE | Zhao, S., Sheety, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Georgelis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Frase, C.M. | | | | MGC clone distribution found through the I.M.A.G.E. Consortium/LINL at: | | |
| AUTHORS | | Rattus | 1 (bases 1 to 789) | | http://image.lnl.gov | | |
| | | Other_GSS: CH230-119L10.TJB | | | Plate: LIAM0733 row: b column: 06 | | |
| | | Contact: Shaying Zhao | | | High quality sequence stop: 683. | | |
| | | Department of Eukaryotic Genomics | | | Location/Qualifiers | | |
| | | The Institute for Genomic Research | | | 1..702 | | |
| | | 9712 Medical Center Dr., Rockville, MD 20850, USA | | | /organism="Homo sapiens" | | |
| | | Tel: 301 838 0200 | | | /db_xref="taxon:9606" | | |
| | | Fax: 301 838 0208 | | | /clone="IMAGE:4823333" | | |
| | | Email: szhaotigr.org | | | /clone_id="NIH_MGC_97" | | |
| | | Copies are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat30.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). | | | /lab_host="DH10B" | | |
| | | Clones may be purchased from BACPAC Resources page: http://www.chori.org/bacpac/ or ering_information.htm). BAC end plate: 119 row: L column: 10 | | | /note="Organ: testis; Vector: pBluescriptR (modified pBluescript RS+); Site_1: BamHI; Site_2: SalI-XbaI (gtcgag oligo-dT primed using primer 5'-TTTTTTTTTTTNTVN-3', size selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." | | |
| | | Seq primer: T7 Class: BAC ends. | | | | | |
| | | | | | BASE COUNT | 137 a | 208 c |
| | | | | | ORIGIN | 238 g | 119 t |
| | | | | | | | |
| FEATURES | | Location/Qualifiers | | | | | |
| | | 1..789 | | | Query Match | 19.3% | Score 35.4; |
| | | /organism="Rattus norvegicus" | | | Best Local Similarity | 53.28; | DB 12; |
| | | /strain="BN/SsNHsd/MCW" | | | Matches | 75; | Length 702; |
| | | /db_xref="taxon:10116" | | | Conservative | 0; | Pred. No. 3 1; |
| | | /clone="CH230-119L10" | | | Mismatches | 66; | Indels 0; |
| | | /clone_id="CHORI-230 Segment 1" | | | Gaps | 0; | |
| | | /seq="Final" | | | | | |
| | | /cell_type="Brain" | | | | | |
| | | /note="Vector: pTARBA2C2.1; Site_1: EcoRI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong" | | | | | |
| | | BASE COUNT | 121 a | 191 c | 217 g | 260 t | |
| | | ORIGIN | | | | | |
| | | | | | | | |
| Query Match | 20.0% | Score 36.6; | DB 17; | Length 789; | Qy | 145 TAGGAAGAGCTATGGCTTGTGTCACCA 144 | |
| Best Local Similarity | 60.6% | Pred. No. 1.4; | | | Db | 543 TGGAAGAGTGACAGTTCCT 523 | |
| Matches 60; | Conservative | 0; | Mismatches | 39; | Indels | 0; | Gaps 0; |
| | | | | | | | |
| Qy | 85 CTATTATCCCCAGTGCCTGGCTGGATGGGAGACGTGACTTCATC 144 | | | | RESULT 6 | | |
| Db | 645 CTTTTCTGGCAAGAGACCTGGCTGGAGAACAGGGACACAGGGAGTCCTC 586 | | | | BF571585 | | |
| | | | | | LOCUS | BF571585 | 831 bp mRNA |
| | | | | | DEFINITION | 602078004F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252465 5' , | |

| | | | |
|------------|---|----------------------------|---|
| ACCESSION | mRNA sequence. | TITLE | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index |
| VERSION | BF571585 | JOURNAL | Unpublished (1997) |
| KEYWORDS | BF571585.1 GI:11645297 | COMMENT | Other ESTs: dc43b12.xl Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov |
| ORGANISM | Homo sapiens | TISSUE | Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NIH-MGC http://mgc.nci.nih.gov/. Unpublished (1999) | LIBRARY PREPARATION | Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. |
| AUTHORS | National Institutes of Health, Mammalian Gene Collection (MGC) | CDNA LIBRARY PREPARATION | Life Technologies, Inc. |
| TITLE | Unpublished (1999) | CDNA LIBRARY ARRANGED BY | The I.M.A.G.E. Consortium (LNLN) |
| JOURNAL | Contact: Robert Strausberg, Ph.D. | DNA SEQUENCING BY | Washington University Genome Sequencing Center |
| COMMENT | Email: cgaps-r@mail.nih.gov | CLONE DISTRIBUTION | Xenopus Clones from this library are available through the I.M.A.G.E. Consortium/LNLN at: infogimage.lnl.gov |
| | Tissue Procurement: ARCC/DCR/DTP | SEQ PRIMER | -40RP from Gibco |
| | CDNA Library Preparation: CLONETECH Laboratories, Inc. | HIGH QUALITY SEQUENCE STOP | High quality sequence stop: 269. |
| | CDNA Library Arranged by: The I.M.A.G.E. Consortium (LNLN) | LOCATION/QUALIFIERS | Location/Qualifiers |
| | DNA Sequencing by: Incyte Genomics, Inc. | FEATURES SOURCE | 1. .283 organism="Xenopus laevis" /db_xref="taxon:8355" /clone="IMAGE:3399886" /clone_1b="NICHD XGC Emb3" /tissue_type="embryo (stages 24-25)" /lab_host="DH10B (phage-resistant)" /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.7 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library." |
| FEATURES | Clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.nih.gov | BASE COUNT | 76 a 58 c 68 g 81 t |
| source | Plate: LNCM1077 row: h column: 02 | ORIGIN | Query Match Score 18.6%; DB 12; Length 283; Best Local Similarity 61.1%; Pred. No. 5.1; Matches 55; Conservative 0; Mismatches 35; Indels 0; Gaps 0; |
| | High quality sequence stop: 571.. | | Qy 63 GCAGAAGAGATGGTGAAGCTATTATGCCAGGCTTCCTGCGGGGTATGG 122 Db 157 GCAGATGAAATTGCTTAAGGCCATTATTCAGCAGGGCAATGCTCCCTGGCTCAT 216 |
| | Location/Qualifiers | | Qy 123 ATGAAAGTGCTGTACTCTAGAAAG 152 Db 217 ATTGTAGAGGCTGTGTAGACAGGAG 246 |
| | 1. .831 | RESULT | RESULT 8 A1512580 |
| | organism="Homo sapiens" | LOCUS | AI512580 695 bp mRNA linear EST 23-APR-2001 |
| | /db_xref="taxon:9606" /clone="IMAGE:252465" | DEFINITION | LD4491.5 prime 1D Drosophila melanogaster embryo port2 Drosophila melanogaster cDNA clone LD4491 5 similar to Cyp310al; FBan0010391 |
| | clone_1b="NIH MGC_62" | SEQUENCE | 'cytochrome P450' located on: 2L 37A3-37A3; 04/10/2001, mRNA sequence. |
| | tissue_type="melanotic melanoma, high MDR" | ACCESSION | A1512580 |
| | /lab_host="DH10B (T1 Phage-resistant)" | VERSION | EST |
| | /note="Organ: skin; Vector: pCR-LIB (Clontech); Site_1: SfI1 (ggccatataggcc); Site_2: SfI1 (ggccatataggcc); double-stranded cDNA was prepared from cell line KNA. 5' | KEYWORDS | EST |
| | and 3' adaptors were used in cloning as follows: 5', adaptor sequence: 5'-ATCTAGAGGGAGGGAGGACAGT-dT(30)Bu-3', sequence: 5'-ATCTAGAGGGAGGGAGGACAGT-dT(30)Bu-3', (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)." | ORGANISM | Drosophila melanogaster |
| BASE COUNT | 219 a 190 c 216 g 206 t | REFERENCES | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Drosophilidae; Drosophila. |
| ORIGIN | | AUTHORS | Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M. |
| | | TITLE | BDGP/HM1 Drosophila EST Project |
| | | JOURNAL | Unpublished (2001) |
| | | COMMENT | On Mar 16, 1999 this sequence version replaced 91:4421998. Other ESTs: LD4491.3 prime Contact: Stapleton, M. |
| RESULT 7 | | DEFINITION | BDGP |
| LOCUS | BG161919 | ACCESSION | Lawrence Berkeley National Lab |
| DEFINITION | 283 bp mRNA linear EST 06-FEB-2001 | VERSION | One Cyclotron Rd, Berkeley, CA 94720, USA |
| ORGANISM | dc43b12.y1 NICHD XGC Emb3 Xenopus laevis cDNA clone IMAGE:3399886 | KEYWORD | Fax: 510 486 6798 |
| | 5', mRNA sequence. | SOURCE | Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu |
| | BG161919 | VERSION | hit genomic AE003659; arm2L [18266373,18507269] |
| | BG161919.1 GI:12695838 | KEYWORD | estimated cyto-36F7-37A1; 04/10/2001 |
| | African clawed frog. | ORGANISM | Plates: LD 444 row: H column: 7 |
| | Xenopus laevis | REFERENCE | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. |
| | Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus. | AUTHORS | |
| | 1 (bases 1 to 283) | | |

| FEATURES | | High quality sequence stop: 585 POLYA-No. | | | |
|------------|---|--|--------------------------------------|----------------|------------|
| | Location/Qualifiers | source | | | |
| | 1. '695 /organism="Drosophila melanogaster" 'ab xlink:href="#taxon_7227" 'clone_id="LD4491" 'clone_lib="LD Drosophila melanogaster embryo porT2" 'sex="male" and female" 'dev_stage="0 to 24 hours mixed stage embryonic" 'lab_host="XLI Blue" 'note="Organ: embryo; Vector: porT2; Site 1: EcoRI; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into porT2." POR2." | | | | |
| BASE COUNT | 171 a | 175 c | 176 g | 173 t | |
| ORIGIN | | | | | |
| Query | CCPAGGGATGCCAGAGATCCAAGTGAGGAATGTTGAGGTATTATCCCC 69; Conservative | Match | 18.4%; Score 33.6; DB 9; Length 695; | | |
| Match | CCAACACGATGTCGGAGANTTCGGCGAGCTCCAGAAAAGGGTGTATTTAAC 400 | Best Local Similarity | 53.9%; Pred. No. 11; | | |
| Matches | | Mismatches | 0; Mismatches | 0; Indels | 0; Gaps 0; |
| Qy | 98 CAGTGCGCTTCCCTGCTGGGCATGGATGAACAGTGGCTCATCTAGAAAGAGCTA 460 ATTGTGCTGGACAGCCAAAGGTGTCACAGGAATGGATATCCACGAAAAACTCA | Db | 158 TGGTTCT 165 | 520 GAGTTT 527 | |
| Qy | | Db | | | |

RESULT 9
 AI243308/C
LOCUS AI243308 mRNA Linear EST 21-DEC-1998
DEFINITION qh41b03_x1l Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847213 3', mRNA sequence.
ACCESSION AI243308
VERSION AI243308.1 GI:3838705
KEYWORDS EST,
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 438)
AUTHORS NCI-CGAP
TITLE http://www.ncbi.nlm.nih.gov/micgcg.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997).
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-r@mail.nih.gov
 This clone is available royalty-free through LInL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
source
 1. 438
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1847213"
 /clone.lib="Scares_NFL_T_GBC_S1"
 /lab_host="DH10B"
QUALIFIERS
 /note="Organ: Pooled; vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung Nb119W, testis NIH, and B-cell
 NCL CGAP GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The was
 was PCR-amplified cDNAs from pools of 5,000 clones made

| | | | | | | |
|--|--|---|------------------------------|------------|-----------------------|---|
| Qy | 101 | TGCCCTCCCTGCTGGGTATGGTGAACAGGGTGACTTCATCT | 145 | | DEFINITION | CH230-186E20.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone |
| Db | 143 | CTCCCTCCCTGCTGGGTATGGGTGAGTTGTTCT | 99 | | ACCESSION | BH68816 |
| | | | | | VERSION | BH68816.1 GI:17181122 |
| | | | | | KEYWORDS | GSS |
| RESULT | 11 | | | | ORGANISM | Rattus norvegicus |
| LOCUS | BH274856 | BH274856 | 481 bp | DNA linear | GSS | 30-NOV-2001 |
| DEFINITION | CH230-48II.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone | | | | REFERENCE | 1 (bases 1 to 594) |
| ACCESSION | BH274856 | CH230-48II.TJ | DNA sequence | | AUTHORS | Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Gear,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M. |
| VERSION | BH274856.1 | GI:17187258 | | | JOURNAL | RAT BAC End Sequences from Library CHORI-230 EcorI segment |
| KEYWORDS | GSS. | | | | COMMENT | Unpublished (1999) |
| SOURCE | Rattus norvegicus | Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | | Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org |
| ORGANISM | Rattus norvegicus | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | | Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@email.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Place: 186 row: E column: 20 Seq primer: T7 Class: BAC ends. |
| REFERENCE | AUTHORS | Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Gear,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M. | | | FEATURES | Location/Qualifiers |
| JOURNAL | TITLE | Rat BAC End Sequences from Library CHORI-230 EcoRI segment | | | source | 1. .594 /organism="Rattus norvegicus" /strain="BN/SNHSd/MCW" /db_xref="taxon:10116" /clone="CH230-186E20" /clone_idb="CHORI-230 Segment 1" /sex="Female" /cell_type="Brain" /note="Vector: PTARBAC2.1; Site_1: EcorI; Site_2: EcoRI; CHORI-230 Rat (BN/SNHSd/MCW) BAC library produced by Pieter de Jong" |
| COMMENT | COMMENT | Unpublished (1999) | | | BASE COUNT | 158 a |
| CONTACT | Other_GSS: | CH230-48II.TV | | | ORIGIN | 187 c 155 g 94 t |
| DEPARTMENT | Shaying Zhao | | | | Query Match | Score 33; DB 17; Length 594; |
| THE INSTITUTE FOR GENOMIC RESEARCH | | | | | Best Local Similarity | 18.0% |
| 9712 MEDICAL CENTER DR., ROCKVILLE, MD 20850, USA | | | | | Matches | 54; Conservative 0; Mismatches 35; Indels 0; Gaps 0; |
| FAX: 301 838 0208 | | | | | Qy | 88 TTATATTCCCCAAGTGCCTTCCTGCTGGCTATGGTGAACAGTCATCTGACTTCATCTAG 147 |
| Email: szhao@tigr.org | | | | | Db | 235 TTCTCGTCAAGAGCTCGCTGTAACAGCACAGGACACAGGAGATTCCTCTAG 294 |
| Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@email.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Place: 48 row: J column: 1 Seq primer: SP6 Class: BAC ends. | | | | | Qy | 148 GAAAGACCTAAGCTTGTCTGCTCCTGGAG 176 |
| LOCATION/QUALIFIERS | 1. .481 | /organism="Rattus norvegicus" /strain="BN/SNHSd/MCW" /db_xref="taxon:10116" /clone="CH230-48II.TJ" /clone_idb="CHORI-230 Segment 1" /sex="Female" /cell_type="Brain" /note="Vector: PTARBAC2.1; Site_1: EcorI; Site_2: EcoRI; CHORI-230 Rat (BN/SNHSd/MCW) BAC library produced by Pieter de Jong" | | | Db | 295 GACCGGGCACTTCCTCGTGTGAG 323 |
| SOURCE | BASE COUNT | 129 a | 141 c 125 g 86 t | | RESULT | 13 |
| ORIGIN | Query Match | 18.0% | Score 33; DB 17; Length 481; | | BM663839 | 582 bp mRNA linear EST 27-FEB-2002 |
| Best Local Similarity | 60.7% | Pred. No. 14; | | | LOCUS | UI-ECL1-afe-k-03-0-UI.s1 UI-ECL1 Homo sapiens cDNA clone |
| Matches | 54; | Conservative 0; Mismatches 35; Indels 0; Gaps 0; | | | DEFINITION | UI-ECL1-afe-k-03-0-UI 3', mRNA sequence. |
| Qy | 88 TTATATTCCCCAAGTGCCTTCCTGCTGGCTATGGTGAACAGTCATCTGACTTCATCTAG 147 | | | | ACCESSION | BM663839 |
| Db | 265 TTCTCGTCAAGAGCTCGCTGTAACAGCACAGGAGATTCCTCTAG 324 | | | | VERSION | BM663839.1 GI:18969506 |
| Qy | 148 GAAAGACCTAAGCTTGTCTGCTCCTGGAG 176 | | | | KEYWORDS | EST. |
| Db | 325 GACCGGGCACTTCCTCGTGTGAG 353 | | | | ORGANISM | Human |
| RESULT | 12 | | | | REFERENCE | 1 (bases 1 to 582) |
| LOCUS | BH268816 | BH268816 | 594 bp | DNA linear | GSS | 30-NOV-2001 |
| | | | | | | |

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA sequence: 11-93, >ALU (matched compliment)
 Seg primer: M13 Forward
 POLYA-refs.

FEATURES

- source 1. 582
 - /organism="Homo sapiens"
 - /db_xref="taxon:9606"
 - /clone="YU-E-CL1-afe-k-03-0-UI"
 - /tissue_type="human retina"
 - /dev_stage="adult"
 - /lab_host="phi10B (Life Technologies) (T1 phage resistant)"
 - /note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a modified poly-linker; Site_1: EcoR I; Site_2: Not I; YU-E-CL1 is a normalized cDNA library containing the following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-PAC vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCC. This library was created for the program Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
 - TAG LIB-UI-E-CL1
 - TAG TISSUE="human retina
 - TAG SEQ=CGCGC"

BASE COUNT 171 a 128 c 98 g 185 t

ORIGIN

Query Match 17.9%; Score 32.8; DB 13; Length 582;
 Best Local Similarity 54.0%; Pred. No. 18;
 Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Query 8 TCCCCCATGTCAGGCCAAAGGGCTCATCCCTAAGGTGTCAGAGATCAAGTGCGACA 67
 Db 149 TCCCTCATCAAGGACAGCTGCTTCATAGTCATGCTATGGCA 90

Query 68 AGGAGAATGTTGAGGTATTATCCCCAGTGCTCCGCTATGGATGA 127
 Db 89 GGCAGGGTTGCACTGAGTCAGTCAGCTGGCCACTGCACTGCGACTGGCAA 30

Query 128 CAGT 131
 Db 29 GACT 26

RESULT 14 CNS0174A/C
LOCUS CNS0174A
DEFINITION Drosophila melanogaster genome survey sequence Sp6 end of BAC

ACCESSION A0543989/c
VERSION A0543989
KEYWORDS A0543989.1 GI:4869383
SOURCE GSS, human.
ORGANISM Homo sapiens
DEFINITION Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 DNA sequence.
ACCESSION A0543989
VERSION A0543989.1 GI:4869383
KEYWORDS A0543989
SOURCE GSS, human.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HOMO.
REFERENCE 1 (bases 1 to 226)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence - Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSS: RPCI-11-357B13.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: hb@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@ejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet CS (info@resgen.com). BAC end search page: http://www.tigr.org/tbdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: T7

Class: BAC ends.

FEATURES source Location/Qualifiers

1. 226
 /organism="Homo sapiens"
 /db_xref="GDB:7636740"
 /db_xref="taxon:9606"
 /clone="RPCI-11-357B13"
 /clone_id="RPCI-11-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; site_1: EcoRI; site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 SE COUNT 58 a 59 g 51 t

ORIGIN

| | Query Match | Score | Length |
|----|---|-------|--------|
| Qy | 17.7% | 32.4 | 226 |
| Db | 64.9% | 14 | |
| Qy | 49 CCAGAGATCCAGTGTGAAAGGAGAATGTGGTGAGGCTATTATGCCCAAGTGCCTCC | 108 | |
| Db | 200 CAAGAGATGAAGTGTGGARGGCCAGGAAAGTCAGGAATTCAATGCCCTGGTCCCTCA | 141 | |
| Qy | 109 CTGCTGGCTATGG | 122 | |
| Db | 140 CTGCTTGTCTTAG | 127 | |

Search completed: May 25, 2003, 04:15:51
 Job time : 1765 secs

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|-------|--|-------|--------|----|------|----------------------|
| 1 | 183 | GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. | 1 | 100 | 0 | 183 | 4 US-09-046-594-49 |
| c 2 | 28.2 | OM nucleic - nucleic search, using sw model | 1 | 15 | 4 | 2846 | 4 Sequence 4, Appli |
| c 3 | 28 | Run on: May 25, 2003, 03:09:47 : Search time 52 Seconds (Without alignments) | 1 | 15 | 3 | 2297 | 4 Sequence 1, Appli |
| c 4 | 27.6 | Title: US-09-660-568-49 | 1 | 15 | 1 | 2367 | 3 Sequence 12, Appli |
| c 5 | 27.4 | Perfect score: 183 | 1 | 15 | 0 | 3243 | 2 Sequence 17, Appli |
| c 6 | 27.4 | Sequence: 1 cacacactcccccattctgaa.....ctgtctccctggaggctcecca 183 | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 7 | 27.4 | Scoring table: IDENTITY_NUC GapP 10.0 , Gapext 1.0 | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 8 | 27 | Searched: 441362 seqs, 15333831 residues | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 9 | 27 | Total number of hits satisfying chosen parameters: 882724 | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 10 | 27 | Minimum DB seq length: 0 | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 11 | 26.6 | Maximum DB seq length: 2000000000 | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 12 | 26.6 | Post-processing: Minimum Match 0% | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 13 | 26 | Maximum Match 100% | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 14 | 26 | Listing first 45 summaries | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 15 | 26 | Database : Issued_Patents_NA:* | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 16 | 26 | 1: /cgns_6/_ptodata/1/ina/5A_COMB.seq:* | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 17 | 26 | 2: /cgns_6/_ptodata/1/ina/5B_COMB.seq:* | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 18 | 26 | 3: /cgns_6/_ptodata/1/ina/6A_COMB.seq:* | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 19 | 26 | 4: /cgns_6/_ptodata/1/ina/6B_COMB.seq:* | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 20 | 25.8 | 5: /cgns_6/_ptodata/1/ina/PCTRUS_COMB.seq:* | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 21 | 25.6 | 6: /cgns_6/_ptodata/1/ina/backfiles1.seq:* | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 22 | 25.4 | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 23 | 25.4 | SUMMARIES | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 24 | 25.4 | 8 | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 25 | 25.4 | Score: 100.0% Best Local Similarity 100.0% Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 26 | 25.4 | Query Match Score 183; DB 4; Length 183; Best Local Similarity 100.0%; Fred. No. 8.6e-56; Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |
| c 27 | 25.4 | Sequence 1, Appli | 1 | 15 | 0 | 3243 | 2 Sequence 6, Appli |

Qy 1 CACACACTCCGCCATTCTGACCCCCAAGAGGCTCATCCCCPAAGGATGTCAGAGATCCAA 60
Db 1 CACACACTCCGCCATTCTGACCCCCAAGAGGCTCATCCCCPAAGGATGTCAGAGATCCAA 60

Qy 61 GTGCAGAGGACAATGGTGGGGTATTTTCCCAGGCGCTCCCGCTGGCTAT 120
Db 61 GTGCAGAGGACAATGGTGGGGTATTTTCCCAGGCGCTCCCGCTGGCTAT 120

Qy 121 GGATGAAACAGGGCTGACTTCATGGAAAGAGCTATGGCTTCCTGTCCTGGAGCTCA 180
Db 121 GGATGAAACAGGGCTGACTTCATGGAAAGAGCTATGGCTTCCTGTCCTGGAGCTCA 180

Qy 181 CCA 183
Db 181 CCA 183

RESULT 2 US-08-915-795-1/C
Sequence 1, Application US/08915795
Patent No. 6235713

GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evanson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast

US-08-915-795-1

Query Match Similarity 15.4%; Score 28.2; DB 4; Length 2846;
Best Local Similarity 59.3%; Pred. No. 2.7; Matches 48; Indels 0; Gaps 0;

Qy 6 ACTCCCCATCTGCCCCAAGGGCTATCCCTAACGGATTCAGAGATCCAAGTGC 65
Db 809 ACTGGTCCCGCTAGCATCTGAGAGTAACCTTCATGGAGCTA 750

Qy 66 GAAGGAGAATGTGTGAGGCT 86

RESULT 3 US-09-471-016-12/C
Sequence 12, Application US/09471016
Patient No. 6316195
GENERAL INFORMATION:
APPLICANT: Frederick, Reid D.
APPLICANT: Tooley, Paul W.
APPLICANT: Bonde, Morris R.
APPLICANT: Knorr, David A.
APPLICANT: Peterson, Gary L.
APPLICANT: Schaad, No. 6316195man W.
TITLE OF INVENTION: An Improved Method for the Detection and Identification of Tilletia indica, the Causal Organism of Karnal Bunt
TITLE OF INVENTION: Disease by PCR
FILE REFERENCE: 0101.98
CURRENT APPLICATION NUMBER: US/09/471,016
CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 2297
TYPE: DNA
ORGANISM: Tilletia indica
US-09-471-016-12

Query Match Similarity 15.3%; Score 28; DB 4; Length 2297;
Best Local Similarity 66.7%; Pred. No. 2.8; Matches 40; Indels 0; Gaps 0;

Qy 19 GAGCCCAAGGGCTATCCCTAACGGATTCAGAGATCCAAGTGCAGGGAGATG 78
Db 312 GAGAGCTGGAGCCCTCCCTAGGGAGCCACAGGTACTATTCGAGAAGGGCG 253

RESULT 4 US-08-988A-17/C
Sequence 17, Application US/08276968A
Patent No. 6015701

GENERAL INFORMATION:
APPLICANT: Pierce, James M.
APPLICANT: Shoreibah, Mohamed G.
APPLICANT: Adler, Beverly
APPLICANT: Fregien, Nevis L.
TITLE OF INVENTION: N-Acetylglucosaminyltransferase V
TITLE OF INVENTION: Proteins and Sequences
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,968A
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/905,795
FILING DATE: 29-JUN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/016,863
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M. 33, 878
 REGISTRATION NUMBER: 34-92D
 REFERENCE/DOCKET NUMBER: 34-92D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089
 TELEX: 49617824
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2367 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 145..2367

Query Match 15.1%; Score 27.6; DB 3; Length 2367;
 Best Local Similarity 48.1%; Pred. No. 4;
 Matches 78; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 9 CCCCCATTCTGAGCCCCAAGGGCTCATCCTAAAGATGTCAGATCCAAAGTGCAGAA 68
 Db 2335 CCTTGATGAGTCTGGCAAGGCAATCTCGTGTGGGTGAC 2276

Qy 69 GGAGATGTTGAGCTTCACTAGCTTCTGGCTGGGGATGGAC 128
 Db 2275 TGAAGAGCAGAGATCCCCTGGGACACAGTCTGGGTAGAAGGATGCCA 2216

Qy 129 AGTGGCTGACTTCATCTAGAAAGAGCTATGGCTCTGCTC 170
 Db 2215 CCAGGATGTCCTGTACAGTCTGAGCTGGAGGTCACTC 2174

RESULT 5
 Sequence 6, Application US/08239276
 GENERAL INFORMATION:
 APPLICANT: Rabin, Daniel
 TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sprung Kramer Schaefer & Briscoe
 STREET: 660 White Plains Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-5144
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.5
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,646
 FILING DATE: 05-MAY-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,646
 FILING DATE: 08-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/239,276
 FILING DATE: 08-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/239,276
 FILING DATE: 08-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/715,181
 FILING DATE: 14-JUN-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/441,703
 FILING DATE: 04-DEC-1989
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/312,543
 FILING DATE: 17-FEB-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurt G. Briscoe
 REGISTRATION NUMBER: 33,141
 REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
 TELECOMMUNICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Kurt G. Briscoe
 REGISTRATION NUMBER: 33,141
 REFERENCE/DOCKET NUMBER: MDI 251.4-KGB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 332-1700
 TELEFAX: (914) 332-1844
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2343 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 145..2367

Query Match 15.0%; Score 27.4; DB 2; Length 3243;
 Best Local Similarity 57.6%; Pred. No. 5 4;
 Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 35 ATCCCTAAGGTGTCAGAGATAAGTGCAGAAAGGAAATGTTGTTGAGGCTTATTATTC 94
 Db 161 ATGTCAGGACCCAGAGGCCCTAGCAGAAAGCTCAGCTTCAGTCTGTGTCATGATTC 220

Qy 95 CCCCCATGCTTCCTCTGGCTTA 119
 Db 221 ACCAGTGTCCACCCCTGGGACCA 245

RESULT 6
 Sequence 6, Application US/08468579B
 GENERAL INFORMATION:
 APPLICANT: Rabin, Daniel
 TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
 TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sprung Kramer Schaefer & Briscoe
 STREET: 660 White Plains Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-5144
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.5
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,579B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/239,276
 FILING DATE: 05-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/715,181
 FILING DATE: 14-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,646
 FILING DATE: 04-DEC-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/441,703
 FILING DATE: 04-FEB-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurt G. Briscoe
 REGISTRATION NUMBER: 33,141
 REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 332-1717
 TELEFAX: (914) 332-1844
 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3243 nucleotide
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 S-08-468-579B-6

| Query Match | Best Local Similarity | 15.0% |
|-------------|-----------------------|---------------------------|
| Matches | 57.6% | |
| 49; | Conservative | |
| y | 35 | ATCCCTTAAGATTGTGCCAGAGAA |
| | 161 | ATGTCAAAGGCACCCAAAGAA |
| b | 95 | CCCCCAGTGGCTTCCTCGTGGCTGG |
| | 221 | ACCAGGTGTCACCCCTGGGG |

RESULT 7

Sequence 6, Application US/08-468-577B-6

Patent No. 6001804

GENERAL INFORMATION:

APPLICANT: Rabin, Daniel
 TITLE OF INVENTION: PANC

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sprung Krammer
 STREET: 660 White Plains
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA

ZIP: 10591-5144

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette,
 COMPUTER: Apple Macintosh,
 OPERATING SYSTEM: System
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US
 FILING DATE: 06-JUN-1994
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US
 FILING DATE: 05-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US
 FILING DATE: 08-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US
 FILING DATE: 14-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US
 FILING DATE: 04-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US
 FILING DATE: 17-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Kurt G. Briscoe
 REGISTRATION NUMBER: 3

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 332-1717
 TELEFAX: (914) 332-1844

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3243 nucleotide

```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-577B-6

Query Match      15.0%; Score 27.4; DB 3; Length 3243;
Best Local Similarity 57.6%; Pred. No. 5, 4;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy   35 ATCCCTAAGGATGCCAGATCCAAGTGCAGAAATGTTGAGGTATTATTC 94
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   161 ATGTCATGGGCCAACCCCTCAGGAAGCTCCAGCTCTGGTCATGTC 220
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   95 CCCAGTGCTCCCTGCTGGCTA 119
    ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db   221 ACCAGCTGTCCCACCCCTCGGGARCCA 245
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-08-724-394A-20/C
Sequence 20, Application US/08724394A
Patent No. 587237

GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724.394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fites, Rehee A. 35,136
REGISTRATION NUMBER: 017957-000100
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match      14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 50 CAGAGATCCAGTGGAGAAATGGTGGAGCTATTATGCCCGAGTCCTCCCC 109
Db 111483 CAGGATGTAGATGCCAAGGAGAGTTATGTACTATCCCTGCATACCCCCC 111424

Qy 110 TGCTGG 116

Db 111423 TGCTGG 111417

RESULT 9
US-08-724-394A-21/C ; Sequence 21, Application US/08724394A
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; ADDRESS: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; NUMBER OF SEQUENCES: 31
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-08-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONFIG"

US-08-724-394A-21

Query Match 14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONFIG"

US-08-724-394A-21

Query Match 14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONFIG"

US-08-724-394A-21

Query Match 14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONFIG"

RESULT 10
US-08-724-394A-22/C ; Sequence 22, Application US/08724394A
; Patent No. 5672237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; ADDRESS: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONFIG"

US-08-724-394A-22

Query Match 14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONFIG"

US-08-724-394A-22

Query Match 14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONFIG"

US-08-724-394A-22

Query Match 14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONFIG"

US-08-724-394A-22

RESULT 11
US-08-016-863-15/C ; Sequence 15, Application US/08016663
; Patent No. 562003
; GENERAL INFORMATION:
; APPLICANT: Pierce, J. M.
; ADDRESS: Shoreibah, Mohamed G.
; CITY: Adler, Beverly L.
; STATE: Fregien, Nevis L.

TITLE OF INVENTION: N-Acetylglucosaminyltransferase V
 TITLE OF INVENTION: Protein and Gene

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner, P.C.
 STREET: 5370 Manhattan Circle, Suite 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: USA

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/016, 863

FILING DATE: 19930210

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/905, 795

FILING DATE: 29-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 34-92D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303)499-8080

TELEFAX: (303)499-8089

TELEX: 623189

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2624 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 299 .. 2521

US-08-016-863-15

Query Match 14.5%; Score 26.6; DB 1; Length 2624;
 Best Local Similarity 48.4%; Pred. No. 9, 5; Indels 0; Gaps 0;
 Matches 74; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

9 CCCCCATTCCTGAGCCCCAGGGCTCATCCCTAAGGATGTCCAGATCCAGTGCAGAA 68
 Db 2489 CCTTGATGAACTCCGGCAGGGCAGATCCGGCTGGCTGGTGGCGCCGGCAAC 2430

Qy 69 GGAAATGGTGGCTATTTATCCCCACTGCCCTGCGCTGGCTGGATGAAC 128
 Db 2429 TGAAGGAGGAGATCCCTGGAACACAGTCGCTCTGGGGTAGAAGGGGCA 2370

Qy 129 AGTGGCGAAGCTCATCTAGGAAAGAGCTATGGAAAAGAGCTTGGC 161
 Db 2369 CCAGGATGTCCTGATAGTCTGAGCTTGGC 2337

RESULT 12
 US-08-276-968A-15/c
 Sequence 15, Application US/08276968A

; Patent No. 6015701

; GENERAL INFORMATION:

; APPLICANT: Pierce, James M.

; APPLICANT: Shoreliah, Mohamed G.

; APPLICANT: Adler, Beverly

; APPLICANT: Fregien, Nevil L.

; TITLE OF INVENTION: N-Acetylglucosaminyltransferase V
 ; NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee and Winner, P.C.
 STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

COUNTRY: USA

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276, 968A

FILING DATE: 19-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/016, 863

FILING DATE: 10-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 34-92D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303)-499-8080

TELEFAX: (303)499-8089

TELEX: 49617824

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2624 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 299 .. 2521

US-08-276-968A-15

Query Match 14.5%; Score 26.6; DB 3; Length 2624;
 Best Local Similarity 48.4%; Pred. No. 9, 5; Indels 0; Gaps 0;
 Matches 74; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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 Db 2489 CCTTGATGAACTCCGGCAGGGCAGATCCGGCTGGTGGTGGCGCCGGCACAC 2430

Qy 69 GGAAATGGTGGCTATTTATCCCCACTGCCCTGCGCTGGCTGGATGAAC 128
 Db 2429 TGAAGGAGGAGATCCCTGGAACACAGTCGCTCTGGGGTAGAAGGGGCA 2370

Qy 129 AGTGGCGAAGCTCATCTAGGAAAGAGCTATGGAAAAGAGCTTGGC 161
 Db 2369 CCAGGATGTCCTGATAGTCTGAGCTTGGC 2337

RESULT 13
 US-09-34-408-1
 Sequence 1, Application US/09434408
 ; Patent No. 644697

; GENERAL INFORMATION:
 ; APPLICANT: Venezia, Domenick
 ; APPLICANT: Grossmann, Angelika
 ; TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
 ; FILE REFERENCE: 98-41
 ; CURRENT APPLICATION NUMBER: US/09/434,408
 ; CURRENT FILING DATE: 1999-11-04
 ; EARLIER APPLICATION NUMBER: US 60/108,258

EARLIER FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 3138
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (367)...(2535)
 US-09-434-408-1

Query Match 14.2%; Score 26; DB 4; Length 3138;
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 Matches 56; Conservative 0; Mismatches 50; Indels 0;
 Gaps 0;

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Qy 68 AGGAAATGGTGAGGTATTATTCCCTCAGTGCCCTTCCTCTGCT 113
 Db 533 AGAAAAGGTGCTGATCCACCTCACGAACTGCACGTCAC 578

RESULT 14
 US-09-209-668-18

Patent No. 6114517
 GENERAL INFORMATION:
 APPLICANT: Monia, Brett P.
 TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
 FILE REFERENCE: ISPH-0336
 CURRENT APPLICATION NUMBER: US/09/209,668A
 CURRENT FILING DATE: 1998-12-10
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 18
 LENGTH: 3834

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (117)...(1949)
 PUBLICACION INFORMATION:
 DATABASE ACCESION NUMBER: M24736/Genbank
 DATABASE ENTRY DATE: 1994-11-07
 -09-209-668-18

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Qy 81 GAGGCTATTATTCCCTCAGTGGCTATGGCTTCCCTGCTGGCTATGGTGAACAGTGGCTGACTT 140
 Db 2132 CTTCACACTGAAAGACTCACTGTTCCCTACTCTAGGATCAAGAAGTGTGGCT 2191

Qy 141 CATCTAGAAAGACCTAT 158
 Db 2192 ATGAAAGGAAAGGATAT 2209

RESULT 15
 US-09-435-470-1
 Sequence 1, Application US/08365470
 Patent No. 5632991
 GENERAL INFORMATION:

APPLICANT: Gimbrone, Jr., Michael A.
 TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
 THEREOF
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 New York Ave., NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/365,470
 FILING DATE: herewith
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/102,510
 FILING DATE: 05-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/850,802
 FILING DATE: 13-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Markowicz, Karen R.
 REGISTRATION NUMBER: 36,351
 REFERENCE/DOCKET NUMBER: 0627.1350003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2500
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3854 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-365-470-1
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 Best Local Similarity 49.3%; Pred. No. 18;
 Matches 68; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
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 Job time : 354 secs

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Gencore version 5.1.4_P5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 03:14:07 ; Search time 125 Seconds

(without alignments)
1933.157 Million cell updates/sec

Title: US-09-660-568-49

Perfect score: 183
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Searched: 828747 seqs, 660231138 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

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13: /cgn2_6_ptodata/2/pubpna/us60_new_pub.seq:*
14: /cgn2_6_ptodata/2/pubpna/us60_pubcomb.seq:*
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Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|---------------------|----|--------------------|
| 1 | 35.2 | 19.2 | 164 | 10 | US-09-864-761-21666 | | Sequence 21666, A |
| c 2 | 30.6 | 16.7 | 5216 | 9 | US-10-125-540-607 | | Sequence 607, App |
| c 3 | 30.6 | 16.7 | 5216 | 9 | US-10-074-095-695 | | Sequence 695, App |
| c 4 | 30.6 | 16.7 | 5216 | 10 | US-09-764-870-607 | | Sequence 607, App |
| c 5 | 30.6 | 16.7 | 5216 | 10 | US-09-764-860-695 | | Sequence 695, App |
| 6 | 28.8 | 15.7 | 8894 | 9 | US-10-092-154-1606 | | Sequence 1606, App |
| 7 | 28.8 | 15.7 | 8894 | 10 | US-09-764-847-1606 | | Sequence 1606, App |
| c 8 | 28.4 | 15.5 | 2001 | 9 | US-09-829-155C-8 | | Sequence 8, Appl |
| c 9 | 28.4 | 15.5 | 2513 | 9 | US-09-829-155C-10 | | Sequence 10, Appl |
| 10 | 28.2 | 15.4 | 358 | 9 | US-10-060-036-1937 | | Sequence 1937, Ap |
| c 11 | 28.2 | 15.4 | 1243 | 12 | US-10-044-090-96 | | Sequence 96, Appl |
| 12 | 28.2 | 15.4 | 1907 | 9 | US-10-023-282-108 | | Sequence 108, App |
| 13 | 28.2 | 15.4 | 2084 | 9 | US-10-023-282-234 | | Sequence 234, App |
| 14 | 28.2 | 15.4 | 2329 | 12 | US-10-044-090-416 | | Sequence 416, App |
| 15 | 27.8 | 15.2 | 374 | 9 | US-09-918-995-6295 | | Sequence 6295, App |
| c 16 | 27.8 | 15.2 | 20907 | 9 | US-09-764-891-996 | | Sequence 996, Ap |
| 17 | 27.8 | 15.2 | 50000 | 9 | US-10-152-724A-20 | | Sequence 20, Appl |
| c 18 | 27.6 | 15.1 | 312 | 10 | US-09-783-590-11431 | | Sequence 11431, A |
| 19 | 27.6 | 15.1 | 945 | 9 | US-10-023-601-43 | | Sequence 43, Appl |

ALIGNMENTS

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RESULT 1
US-09-864-761-21666
; Sequence 21666, Application US-09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanelz, David K.
; APPLICANT: Chen, Wenshang
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US-09-864-761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US-60-180-312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US-60-207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US-09-632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB-24263-6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US-60-236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT-US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT-US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT-US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT-US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT-US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT-US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT-US01/00661
; PRIOR FILING DATE: 2001-01-30
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RESULT 3
 PCT/US01/00670
 US-10-074-095-695
 Sequence 695; Application US/10074095
 Publication No. US20030077704A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PCT08C1
 CURRENT APPLICATION NUMBER: US/10/074,095
 CURRENT FILING DATE: 2002-02-14
 PRIOR APPLICATION NUMBER: 09/764,860
 PRIOR FILING DATE: 2001-01-17
 PRIOR APPLICATION NUMBER: 60/179,065
 PRIOR FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: 60/180,628
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: 60/214,886
 PRIOR FILING DATE: 2000-06-28
 PRIOR APPLICATION NUMBER: 60/217,487
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,758
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/220,963
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/217,496
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,447
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/218,290
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/225,757
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/226,868
 PRIOR FILING DATE: 2000-08-22
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 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/225,267
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/216,880
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/225,270
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/251,869
 PRIOR FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: 60/235,834
 PRIOR FILING DATE: 2000-09-27
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: 60/234,223
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 PRIOR APPLICATION NUMBER: 60/228,924
 PRIOR FILING DATE: 2000-08-30
 PRIOR APPLICATION NUMBER: 60/224,518
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/236,369
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 PRIOR APPLICATION NUMBER: 60/224,519
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 PRIOR APPLICATION NUMBER: 60/220,964
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/241,809
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/249,299
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/236,327
 PRIOR FILING DATE: 2000-09-39
 PRIOR APPLICATION NUMBER: 60/241,785
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/244,617
 PRIOR FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: 60/225,268
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/236,368

RESULT 3
 PCT/US01/00670
 US-10-074-095-695
 Sequence 695; Application US/10125540
 Publication No. US20030059873A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PCT14C1
 CURRENT APPLICATION NUMBER: US/10/125,540
 CURRENT FILING DATE: 2002-04-19
 FILED Application Removed - See File Wrapper or Palm
 NUMBER OF SEQ ID Nos: 646
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 607
 LENGTH: 5216
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-125-540-607

Query Match 19.2%; Score 35.2; DB 10; Length 164;
 Best Local Similarity 71.9%; Pred. No. 0.006; Indels 0; Gaps 0;
 Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 52 GAGATCCAAGTCAGAGGAATGTTGGCTATTATTCCTCCAGTGCCTCCCTCG 111
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Qy 112 CCGG 115
 Db 160 TGGG 163

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 Best Local Similarity 56.4%; Pred. No. 0.92; Indels 0; Gaps 0;
 Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Qy 83 GGCTTATTATCCCTCAAGTCCCTGGATGGAT 123
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; PRIOR FILING DATE: 2000-12-08
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; PRIOR APPLICATION NUMBER: 60/229, 509
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; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231, 243
; PRIOR FILING DATE: 2000-09-08

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| Db | 2738 GAGCTAGATTGCGCACTCAGCTGGCAACAGA | 123 | 123 | Gaps |
| QY | 83 GGCTATTATCCCGAGTGCCTCCCTGGCTATGAA | 2737 | 123 | |
| Db | 2738 GAGCTAGATTGCGCACTCAGCTGGCAACAGA | 2778 | 123 | |

RESULT 4
US-09-764-870-607/C
; Sequence 607, Application US/09764870

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; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; NUMBER OF SEQ ID NOS: 646
; FILE REFERENCE: PT2.14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 607
; LENGTH: 5216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-607

Query Match 16.7%; Score 30.6%; DB 10; Length 5216;
Best Local Similarity 56.4%; Pred. No. 0.92; Indels 0; Gaps 0;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Db 23 CCGAAGGCTCATCCCTAAGGTGTCAGAGTCCAAGTGCAAGGGAAATGGTGA 82
Db 2539 CTGGGAGGCTTAAGCAGGAAATGGTGTAAACCGGAAGGCAAGCTGCAGT 2480
Qy 83 GGCTATTATTCCCCAAGTNGCCTTCCTGGCTATGGA 123
Db 2479 GAGCTTAGATTGGCCACATGCACTCCAGSCTGGCAACAGA 2439
RESULT 5
US-09-764-860-695
; sequence 695, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 665
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-695

Query Match 16.7%; Score 30.6%; DB 10; Length 5216;
Best Local Similarity 56.4%; Pred. No. 0.92; Indels 0; Gaps 0;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Db 23 CCGAAGGCTCATCCCTAAGGTGTCAGAGTCCAAGTGCAAGGGAAATGGTGA 82
Db 2678 CTGGGAGGCTTAAGCAGGAAATGGTGTAAACCGGAAGGCAAGCTGCAGT 2737
Qy 83 GGCTATTATTCCCCAAGTNGCCTTCCTGGCTATGGA 123
Db 2738 GAGCTTAGATTGGCCACATGCACTCCAGSCTGGCAACAGA 2778
RESULT 6
US-10-092-154-1606
; Sequence 1606, Application US/10092154
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC00961
; CURRENT APPLICATION NUMBER: US/10/092,154
; NUMBER OF SEQ ID NOS: 2003
; CURRENT FILING ID: 2002-03-07
; Prior Application removed - See File Wrapper or Palm
; Software: FastSEQ for Windows Version 3.0
; SEQ ID NO: 8
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-829-155C-8

Query Match 15.7%; Score 28.8%; DB 9; Length 8894;
Best Local Similarity 58.0%; Pred. No. 5; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 66 GAAGGAGATGGTGAAGCTTATCCCCAGTGGCTTGCCTGGCTATGGATG 125
Db 3269 GAGGCAGGGTGCAGTAAGTGAACACTGACTCTAGGCTGGTACAGGCC 3328
Qy 126 AACAGTGGCTGACTTCATCTAGAAAGA 153
Db 3329 GACAGCAAGACTTCATCTAGAAAGA 3356
RESULT 7
US-09-764-847-1606
; sequence 1606, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 106
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1606

Query Match 15.7%; Score 28.8%; DB 10; Length 8894;
Best Local Similarity 58.0%; Pred. No. 5; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 66 GAAGGAGATGGTGAAGCTTATCCCCAGTGGCTTGCCTGGCTATGGATG 125
Db 3269 GAGGCAGGGTGCAGTAAGTGAACACTGACTCTAGGCTGGTACAGGCC 3328
Qy 126 AACAGTGGCTGACTTCATCTAGAAAGA 153
Db 3329 GACAGCAAGACTTCATCTAGAAAGA 3356
RESULT 8
US-09-829-155C-8/C
; Sequence 8, Application US/09829155C
; Patent No. US2002015561A1
; GENERAL INFORMATION:
; APPLICANT: Thayer, Edward C.
; TITLE OF INVENTION: Mammalian Disulfide Core Protein-4
; FILE REFERENCE: 00-29
; CURRENT APPLICATION NUMBER: US/09/829,155C
; CURRENT FILING DATE: 2002-04-03
; PRIORITY APPLICATION NUMBER: 60/196,230
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 8
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-829-155C-8

Query Match 15.5%; Score 28.4%; DB 9; Length 2001;

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Best Local Similarity 58.1%; Pred. No. 4.2;
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 98 CAGTGCCCTTCCCTGCTGGCTATCGTGAACAGTGGCAGTCATCTAGAAAGAGCTA 157
Db 305 CACAGACTCCCTGAGACTGCTACGAGTCAAGTAAGGAAAGAAAGATGATCT 246
Qy 158 TGGCTTCGTCCTCTGGACCTACCA 183
Db 245 TAGCTCCCTCATGTGCTCTACTGGCA 220

RESULT 9
US-09-829-155C-10/C
; Sequence 10, Application US/09829155C
; GENERAL INFORMATION:
; APPLICANT: Thayer, Edward C.
; TITLE OF INVENTION: Mammalian Disulfide Core Protein-4
; FILE REFERENCE: 00-29
; CURRENT APPLICATION NUMBER: US/09/829,155C
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/196,230
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-829-155C-10

Query Match 15.5%; Score 28.4; DB 9; Length 2513;
Best Local Similarity 58.1%; Pred. No. 4.5;
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 98 CAGTGCCCTTCCCTGCTGGCTATCGTGAACAGTGGCAGTCATCTAGAAAGAGCTA 157
Db 1281 CACAGACTCCCTGAGACTGCTACGAGTCAAGTAAGGAAAGAAAGATGATCT 1222
Qy 158 TGGCTTCGTCCTCTGGACCTACCA 183
Db 1221 TAGCTCCCTCATGTGCTCTACTGGCA 1196

RESULT 11
US-10-044-090-96/C
; Sequence 96, Application US/10044090
; Patent No. US2002137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028-US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 96
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2002137081A1 1404669CB1
; US-10-044-090-96

Query Match 15.4%; Score 28.2; DB 12; Length 1243;
Best Local Similarity 59.3%; Pred. No. 4.2;
Matches 48; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 6 ACTCCGCCATTCTGAGCCCCAAGGGCTATCCCTAAGGATGTCCAGAGATCCAGTGCA 65
Db 207 ACTGCTCCGGCTGACACTGAGAGTAACCTCTGGAGCACCCATATCGGGTCTA 148
Qy 66 GAAGGAAATGTGGAGGT 86
Db 147 AAAAGAGAGTGTCTGATGCT 127

RESULT 12
US-10-023-282-108
; Sequence 108, Application US/10023282
; Publication No. US20030092853A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ00751
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06

RESULT 10
US-10-060-036-1937
; Sequence 1937, Application US/10060036
; Publication No. US2003007314A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Repler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: 210121-566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1937
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-060-036-1937

Query Match 15.4%; Score 28.2; DB 9; Length 358;
Best Local Similarity 61.6%; Pred. No. 2.7;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

1 / EARLIER APPLICATION NUMBER: 60/048,884
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,894
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,882
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,971
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,964
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,894
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,899
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,964
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,900
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,901
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,893
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,900
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,901
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,892
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,915
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/049,019
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/049,019
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/049,016
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/049,373
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,875
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/049,374
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/049,317
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,949
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/049,374
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,883
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,897
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,898
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,962
 1 / EARLIER FILING DATE: 1997-06-06
 1 / EARLIER APPLICATION NUMBER: 60/048,963
 1 / EARLIER FILING DATE: 1997-12-18
 1 / EARLIER APPLICATION NUMBER: 60/092,921
 1 / EARLIER FILING DATE: 1998-07-15
 1 / EARLIER APPLICATION NUMBER: 60/094,657
 1 / NUMBER OF SEQ ID NOS: 1227
 1 / SOFTWARE: PatentIn Ver. 2.0
 1 / SEQ ID NO: 108
 1 / LENGTH: 1907
 1 / TYPE: DNA
 1 / ORGANISM: Homo sapiens
 1 / US-10-023-282-108

QY 53 AGATCCAACTGGAGAAGGAAATGTGGCAGGGCTTATTCCCCCAAGTGCCCTTCGCCCTGC 112
Db 1159 AGATGGAGGGAGGGAGGGCTGAGTTGGGTTGAATCCCCGGCTCCACCTGC 1654
QY 1113 TGGCTATGGATG 125
Db 1655 AGCATCAAGGTG 1667

RESULT 13
US-10-023-282-234 ; Sequence 234, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ00/P1
; CURRENT APPLICATION NUMBER: US/10/023, 282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205, 258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048, 885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 919
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 972

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 234
; LENGTH: 2084
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: SITE
; LOCATION: (2080)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2080)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2083)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-023-282-234
; Query Match 15.4%; Score 28.2; DB 9; Length 2084;
; Best Local Similarity 61.6%; Pred. No. 5;
; Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 53 AGATCCAAGTGCAGAAGGAAATGGCTATTATCCCCAAGTCCTTCCTCC 112
Db 1780 AGAATGGAGAGGAGCTGAGTTGGGTATTGATCCCCGGTCCACCTC 1839
Qy 113 TGGCTATGATG 125
Db 1840 AGCATCAAGGTTG 1852
; Software: PERL program
; Seq ID No: 416
; Length: 2329;
; Query Match 15.4%; Score 28.2; DB 12; Length 2329;
; Best Local Similarity 61.6%; Pred. No. 5.2;
; Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 53 AGATCCAAGTGCAGAAGGAAATGGCTATTATCCCCAAGTCCTTCCTGC 112
Db 2048 AGAATGGAGAGGAGGAGCTGAGTTGGGTATTGATCCCCGGTCCACCTG 2107
Qy 113 TGGCTATGATG 125
Db 2108 AGCATCAAGGTTG 2120
RESULT 15
US-09-918-995-6295
; Sequence 6295, Application US/09918995
; Publication No. US200300736341
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 6295
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-6295
; Query Match 15.2%; Score 27.8; DB 9; Length 374;
; Best Local Similarity 51.2%; Pred. No. 3.9;
; Matches 65; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
Qy 52 GAGATCCAAGTGCAGAAGGAAATGGCTATTATCCCCAAGTCCTTCCTGC 111
Db 99 GAGGCCAGGGCGGATGCCAGCAGGGGGTACACACACCCGCTGCCTCC 158
; Query Match 15.2%; Score 27.8; DB 9; Length 374;
; Best Local Similarity 51.2%; Pred. No. 3.9;
; Matches 65; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
Qy 112 CTGGCTATGGATGAACTGGCTACATCTAGGAAGAGCTATGGCTTCCTCC 171
Db 159 CGTGTCTGCCTGAGCTGCTCTGGCCCTACACCAGGGTGGACTGGCTCC 218
Qy 172 TGGACT 178
Db 219 AGGACCT 225

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Search completed: May 25, 2003, 04:19:26
 Job time : 142 secs

RESULT 14
 US-10-044-090-416
 ; Sequence 416, Application US/10044090
 ; Patent No. US20030137081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olga Bandman
 ; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
 ; FILE REFERENCE: PA-0028 US
 ; CURRENT APPLICATION NUMBER: US/10/044,090
 ; CURRENT FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 850

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| FEATURES | Location/Qualifiers |
|---|--|
| source | .183 /organism="unknown" |
| BASE COUNT | 43 a 52 c 45 g 43 t |
| ORIGIN | |
| Query Match | 100.0% Score 183; DB 6; Length 183; |
| Best Local Similarity | 100.0% Pred. No. 3e-49; |
| Matches | 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 CACACACTCCCATTCAGCCCCAAGAGCTATCCCTAAGGATGTCAGAGATCCA 60 |
| Db | 1 CACACACTCCCATTCAGCCCCAAGAGCTATCCCTAAGGATGTCAGAGATCCA 60 |
| Qy | 61 GTGCCGAAGGAGAAATGGTGAGGCCATTATTATCCTTAAGGCTATCCCTAAGGATGTCAGAGATCCA 60 |
| Db | 61 GTGCCGAAGGAGAAATGGTGAGGCCATTATTATCCTTAAGGCTATCCCTAAGGATGTCAGAGATCCA 60 |
| Qy | 121 GGATGAACTGGCTGACTTCATCTAGGAAAGACCTATGGCTTCCTGTCAGGCTCA 180 |
| Db | 121 GGATGAACTGGCTGACTTCATCTAGGAAAGACCTATGGCTTCCTGTCAGGCTCA 180 |
| Qy | 181 CCA 183 |
| Db | 181 CCA 183 |
| RESULT 2 | |
| ALI62253_c | ALI62253 |
| LOCUS | 146327 bp DNA linear PRI 21-MAR-2001 |
| DEFINITION | Human DNA sequence from clone RP11-574F11 on chromosome 9, complete sequence. |
| ALI62253 | |
| ALI62253.17 | GI:13677203 |
| HTG | |
| human. | |
| ORGANISM | Homo sapiens |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo | |
| AUTHORS | Clark, G. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (20-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk |
| REFERENCE | requests: clonerequest@sanger.ac.uk |
| COMMENT | On Apr 19, 2001 this sequence version replaced gi:12639553. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred Quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emi, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RP11-574F11 is from the library RCF1-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: PBACE3_6 |
| IMPORTANT: | This sequence is not the entire insert of clone |

RP11-574F11. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-574F11 is at 146327 in this sequence. The true left end of clone RP11-635N21 is at 62948 in this sequence. The true right end of clone RP11-12D24 is at 100.

RP11-574F11. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-574F11 is at 146327 in this sequence. The true left end of clone RP11-635N11 is at 62948; this sequence. The true right end of clone RP11-12D24 is at 10135.

| FEATURES | source |
|------------|----------|
| mlsc_ff | |
| mlsc_ff | |
| BASE COUNT | |
| ORIGIN | |
| Query Mat. | |
| Best Loca. | |
| Matches | |
| Qy | 2 |
| | |
| Db | 145681 A |
| Qy | 62 T |
| | |
| Db | 145621 T |
| Qy | 122 G |
| | |
| Db | 145561 G |
| RESULT | 3 |
| AC09564/c | |
| LOCUS | |
| DEFINITION | |
| ACCESSION | |
| VERSION | |
| KEYWORDS | |
| SOURCE | |
| ORGANISM | |
| REFERENCE | |
| AUTHORS | |
| TITLE | |
| JOURNAL | |
| REFERENCE | |
| AUTHORS | |
| TITLE | |
| JOURNAL | |
| REFERENCE | |
| AUTHORS | |
| TITLE | |
| JOURNAL | |
| COMMENT | |

Drafting Center: SC
 ----- Project Information
 Center project name: chr-1
 Center clone name: RP1-359A17 (sc0138)
 ----- Summary Statistics
 Sequencing vector: Plasmid; L08752; 91% of reads
 Sequencing vector: Plasmid; 9% of reads
 Chemistry: Dye-terminator ET; 40% of reads
 Chemistry: Dye-terminator Big dye; 60% of reads
 Assembly program: Phrap; version 0.900319
 Consensus quality: 189343 bases at least Q40
 Consensus quality: 189424 bases at least Q30
 Consensus quality: 189508 bases at least Q20
 Insert size: 189509; sum-of-contigs
 Quality coverage: 6.9x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': Mapping in progress
 3': RP1-455110 AL357499, 57084-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector. In order to accurately represent the entire circular BAC, small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BamHI

HindIII

KpnI

SmaI

XbaI

XbaII

XbaIII

XbaIV

XbaV

XbaVI

XbaVII

XbaVIII

XbaIX

XbaX

XbaXI

XbaXII

XbaXIII

XbaXIV

XbaXV

XbaXVI

XbaXVII

XbaXVIII

XbaXIX

XbaXX

XbaXXI

XbaXXII

XbaXXIII

XbaXXIV

XbaXXV

XbaXXVI

XbaXXVII

XbaXXVIII

XbaXXIX

XbaXXX

XbaXXI

XbaXXII

XbaXXIII

XbaXXIV

XbaXXV

XbaXXVI

XbaXXVII

XbaXXVIII

XbaXXVIX

XbaXXVII

XbaXXVIII

| TITLE JOURNAL | | TITLE JOURNAL | | TITLE JOURNAL | | TITLE JOURNAL | | TITLE JOURNAL | |
|--|--|---|--|--|--|---|--|---|-------------------|
| REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS | REFERENCE AUTHORS |
| ROY, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnex, C., Spencerman, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talanass, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M. | Direct Submission Submitted (14-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 167115) | Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chopek, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelis, C., LaRoque, K., Lamazares, R., Landers, T., Lebovitz, J., Levine, R., Lindblad-Toh, K., Liu, G., Liu, J., MacLennan, C.H., Marquis, N., McElroy, P., O'Neil, D., Olver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollita, V., Raymond, C., Repta, R., Riebeck, M., Riley, R., Riese, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talanass, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. | Direct Submission Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 167115) | Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chopek, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Govertse, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Keells, C., LaRoque, K., Lamazares, R., Landers, T., Lebovitz, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menes, L., Menes, L., Mihova, T., Milenga, V., Murphy, T., Taylor, J., Nguyen, C., Nicol, R., Norman, C.H., Norman, C.H., O'Connell, P., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riebeck, M., Riley, R., Riese, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talanass, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. | Direct Submission Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 5 (bases 1 to 167115) | Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chopek, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Govertse, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Keells, C., LaRoque, K., Lamazares, R., Landers, T., Lebovitz, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., | Direct Submission Submitted (31-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 5 (bases 1 to 167115) | Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chopek, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Govertse, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Keells, C., LaRoque, K., Lamazares, R., Landers, T., Lebovitz, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., | |

| ACCESSION | AC087354 | GI: | 22450687 | JOURNAL | |
|---|---|---------------|-----------------|---------|--|
| VERSION | HTGS_PHASE2; | HTGS_FULLTOP; | HTGS_ACTIVEFIN. | | |
| WORDS | | | | | |
| HUMAN | | | | | |
| ORGANISM | <i>Homo sapiens</i> | | | | |
| REFERENCE | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Romiidae; Homo. | | | | |
| AUTHORS | 1 (bases 1 to 184787) | | | | |
| TITLE | Birren,B.,Nusbaum,C. and Lander,E. | | | | |
| UNPUBLISHED | <i>Homo sapiens</i> chromosome 8, clone RP1-398H6 | | | | |
| 2 (bases 1 to 184787) | | | | | |
| Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukigalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewart,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Ferreria,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Goettet,M., Graham,L., Grand-Pierre,N., Hapos,B., Headford,A., Horton,L., Huime,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T., Lenchocky,J., Levine,R., Liu,G., MacLean,C., McDonald,P., Marquis,N., Matthews,C., McEwan,P., McCarthy,M., McNeus,L., McNeil,J., McPheeters,R., Meldrum,J., Meneus,L., Mlenga,V., Nguyen,J., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phankhang,P., Pierre,N., Pollara,V., Raymond,C., Rettar,R., Riley,R., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Songuez,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Strassn,J., Subramanian,A., Talanias,J., Testafay,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Vieil,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. | | | | | |
| Direct Submission | | | | | |
| Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA | | | | | |
| 3 (bases 1 to 184787) | | | | | |
| Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukigalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Cooke,P., Cooke,P., DeArellano,K., Dewart,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Grand-Pierre,N., Gage,D., Galagan,J., Garofyn,S., Gord,S., Graham,L., Hagos,B., Huime,W., Iliev,I., Jones,C., Kamat,A., Kortats,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrum,J., Meneus,L., Mlenga,V., Murphy,T., Nguyen,J., Nicol,R., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phankhang,P., Pierre,N., Raymond,C., Rettar,R., Riese,C., Rogov,P., Ronan,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talamas,J., Testafay,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Vieil,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. | | | | | |
| COMMENT | | | | | |
| JOURNAL | | | | | |
| REFERENCE | Submitted (23-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA | | | | |
| AUTHORS | On Aug 23, 2002 this sequence version replaced g1:22297025. | | | | |
| ALL REPEATS | All repeats were identified using RepeatMasker. | | | | |
| PROJECT | Smit,A.F.A. & Green, P. (1996-1997) | | | | |
| WEBSITE | http://ftp.genome.washington.edu/RM/RepeatMasker.html | | | | |
| CENTER | Whitehead Institute/ MIT Center for Genome Research | | | | |
| Center code: WIBR | | | | | |
| Web site: http://www-seq.wi.mit.edu | | | | | |
| CONTACT | Contact: sequence_submissions/genome.w1.mit.edu | | | | |
| CENTER PROJECT NAME | L11709 | | | | |
| CENTER CENTER CLONE NAME | 398_H_6 | | | | |
| NOTE | This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs | | | | |
| are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. | | | | | |
| This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. | | | | | |
| base 1 to 184787) * 1 * 79727 79826: gap of 100 bp * 79827 184787: contig of 104961 bp in length. | | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1. .organism="Homo sapiens" | | | | |
| | /db_xref="taxon:3606" | | | | |
| | /chromosome="8" | | | | |
| | /map="8" | | | | |
| | /clone="RP1-398H6" | | | | |
| | /clonetab="RPCT-11 Human Male BAC" | | | | |
| BASE COUNT | 54973 a 39178 c 39320 g 51130 t 186 others | | | | |
| ORIGIN | | | | | |
| Query Match | 23.7% | | | | |
| Best Local Matches | 72.7% | | | | |
| Similarity | 56; | | | | |
| Conservative | 0; | | | | |
| Mismatches | 21; | | | | |
| Indels | 0; | | | | |
| Gaps | 0; | | | | |
| RESULTS | 8 | | | | |
| AC021973 | 185420 bp DNA linear | | | | |
| LOCUS | RP1-398H6, WORKING DRAFT SEQUENCE, | | | | |
| DEFINITION | Homo sapiens chromosome 8 clone | | | | |
| AC021973 | 7 unorderd pieces. | | | | |
| ACCESSION | AC021973..3 GI:9954353 | | | | |
| VERSION | HGVS-DRAFT. | | | | |
| KEYWORDS | HGVS; PHASE1; | | | | |
| SOURCE | Homo sapiens | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| 1 (bases 1 to 185420) | | | | | |
| REFERENCE | Waterson,N.R. | | | | |
| AUTHORS | The sequence of <i>Homo sapiens</i> clone | | | | |
| TITLE | Unpublished | | | | |
| JOURNAL | 2 (bases 1 to 185420) | | | | |
| REVIEWERS | Waterson,N.R. | | | | |
| AUTHORS | Direct Submission | | | | |
| TITLE | Submitted (22-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108 USA | | | | |
| JOURNAL | On Jul 7, 2000 this sequence version replaced g1:7191944. | | | | |
| COMMENT | Genome Center | | | | |
| JOURNAL | Center: Washington University Genome Sequencing Center | | | | |
| REMARKS | Center code: WUGSC | | | | |
| | Web site: http://genome.wustl.edu/gsc/index.shtml | | | | |
| | Assembly program: Phrap; version 0.900319 | | | | |
| | Consensus quality: 181383 bases at least 040 | | | | |
| | Consensus quality: 183463 bases at least 020 | | | | |
| | Summary Statistics | | | | |
| | Sequencing vector: M13, 898 | | | | |
| | Center: Washington University Genome Sequencing Center | | | | |
| | Center code: WUGSC | | | | |
| | Chemistry: Dye-primer ET; 89% of reads | | | | |
| | Assembly program: Phrap; version 0.900319 | | | | |
| | Consensus quality: 181383 bases at least 040 | | | | |
| | Consensus quality: 183463 bases at least 020 | | | | |

Insert size: 185000; agarose-fp
 Insert size: 184820; sum-of-contigs
 Quality coverage: 6.44 in Q20 bases; agarose-fp
 Quality coverage: 5.98 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 2842: contig of 2842 bp in length
 * 2942: gap of unknown length
 * 2943 6917: contig of 3975 bp in length
 * 6918 7019: gap of unknown length
 * 7018 15680: contig of 8663 bp in length
 * 15681 15780: gap of unknown length
 * 15781 30574: contig of 14/94 bp in length
 * 30575 30674: gap of unknown length
 * 30675 61322: contig of 30648 bp in length
 * 61323 61422: gap of unknown length
 * 61423 93101: contig of 31679 bp in length
 * 93102 93202: gap of unknown length
 * 93202 185420: contig of 92219 bp in length.

FEATURES

source 1..185420 Location/Qualifiers

source /note="assembly_name:Contig8
 /db_xref="taxon:9606"
 /chromosome="8"
 /clone="RP11-338H6"

misc_feature 2943..6917 vector_side:right"
 misc_feature 7018..15680 "note="assembly_name:Contig10"
 misc_feature 15781..30574 "note="assembly_name:Contig11"
 misc_feature 30675..61322 "note="assembly_name:Contig12"
 misc_feature 61423..93101 "note="assembly_name:Contig13
 misc_feature 93202..185420 "note="assembly_name:Contig14"
 misc_feature 53244..a 39520 c 39207 g 52848 t

BASE COUNT

Query Match 23.7% Score 43.4; DB 2; Length 185420;
 Best Local Similarity 72.7%; Pred. No. 0.0029;
 Matches 56; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 65 AGGGAGGATGGGTGAGGCGATTATCCCCCACTGGCCATTGGAT 124
 Db 167596 AGAACAGAGGGATCAGGCCATTGTACCAAAAGTCCCTCTGCCTAAGCTT 167537

Qy 125 GAAGATGGCTGACTTC 141
 Db 167536 TCAAGTGCTTCCTTC 167520

ORIGIN

Query Match 23.7% Score 43.4; DB 2; Length 185420;
 Best Local Similarity 72.7%; Pred. No. 0.0029;
 Matches 56; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 65 AGGGAGGATGGGTGAGGCGATTATCCCCCACTGGCCATTGGAT 124
 Db 167596 AGAACAGAGGGATCAGGCCATTGTACCAAAAGTCCCTCTGCCTAAGCTT 167537

RESULT 9

AC013751 DNA 205816 bp linear PRI 07-MAY-2001
 DEFINITION Homo sapiens chromosome , clone RP11-298P6, complete sequence.

LOCUS AC013751 Homo sapiens chromosome , clone RP11-298P6, complete sequence.

ACCESSION AC013751.6 GI:13958504

VERSION HTNG

KEYWORDS

TITLE Direct Submission
JOURNAL Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On May 6, 2001 this sequence version replaced gi:11094844.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
Center Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
 Center project name: L2369
 Center clone name: 298_P_6

| FEATURES | source | Location/Qualifiers |
|---------------|--------|---|
| repeat_region | | .205816 "Homo sapiens" <i>/organism="Homo sapiens"</i> <i>/ab_xref="taxon:9006"</i> |
| repeat_region | | /clone "RP1-298P6" <i>/clone_lib="RPCI-11 Human Male BAC"</i> |
| repeat_region | | complement(891..1189) <i>/rpt_family="AluJb"</i> <i>/complement(1411..1711)</i> |
| repeat_region | | /rpt_family="AluSq" 3136..3793 "TCTA)n" <i>/rpt_family="TCTA)n"</i> |
| repeat_region | | complement(3794..3914) <i>/rpt_family="FLAM_C"</i> |
| repeat_region | | 3915..4277 "AluUJb" <i>/rpt_family="AluUJb"</i> |
| repeat_region | | complement(4315..4526) <i>/rpt_family="L1MC5"</i> |
| repeat_region | | 4569..4612 "CT-rich" <i>/rpt_family="CT-rich"</i> |
| repeat_region | | 4694..4797 "FAM" <i>/rpt_family="FAM"</i> |
| repeat_region | | complement(4827..5088) <i>/rpt_family="L1MC5"</i> |
| repeat_region | | 5089..5389 "AlusX" <i>/rpt_family="AlusX"</i> |
| repeat_region | | complement(5390..6045) <i>/rpt_family="L1MC5"</i> |
| repeat_region | | 6107..6364 "AlusX" <i>/rpt_family="AlusX"</i> |
| repeat_region | | 6912..6982 "TARGn" <i>/rpt_family="TARGn"</i> |
| repeat_region | | complement(6988..7072) <i>/rpt_family="L1MC5"</i> |
| repeat_region | | 8649..8703 "AlusX" <i>/rpt_family="AlusX"</i> |
| repeat_region | | 8703..8734 "(TC)n" <i>/rpt_family="(TC)n"</i> |
| repeat_region | | 8810..9110 "CA)n" <i>/rpt_family="CA)n"</i> |
| repeat_region | | 9241..9277 "AlusX" <i>/rpt_family="AlusX"</i> |
| repeat_region | | complement(9310..10348) <i>/rpt_family="L1MC5"</i> |
| repeat_region | | complement(10376..110678) <i>/rpt_family="AlusX"</i> |
| repeat_region | | 11057..111087 "AT-rich" <i>/rpt_family="AT-rich"</i> |
| repeat_region | | 11126..111660 "AT-rich" <i>/rpt_family="AT-rich"</i> |
| repeat_region | | 11183..111956 "MIR3" <i>/rpt_family="MIR3"</i> |
| repeat_region | | 12137..12438 "AluJb" <i>/rpt_family="AluJb"</i> |
| repeat_region | | 13183..13359 "TNTATGn" <i>/rpt_family="TNTATGn"</i> |

VERSION AC016675.4 GI:7259724
 SOURCE HTGS_PHASE1; HTGS_DRAFT.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Unpublished
 1 (bases 1 to 174380)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens, clone RP11-699A7

REFERENCE Birren, B., Linton, L., Nusbaum, C., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckrly, R., Boguslavskiy, L., Boukhgalter, B., Brown, A., Castle, A., Colaianno, K., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Horton, L., Galagna, J., Gately, S., Grant, G., Hagos, B., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kahn, L., Marquis, N., Lehoczyk, J., Lieu, C., Locke, K., McDonald, P., McLaughlin, J., McRae, P., McKurt, A., McNear, K., McLaughlin, J., McLeod, J., McRae, P., McNear, K., McRae, P., McNear, C.H., O'Connor, T., O'Donnell, I.P., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, I.P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.J., Tesfaye, S., Tirrell, A., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

JOURNAL Direct Submission

COMMENT Submitted (20-Nov-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02111, USA
 On Mar 17, 2000 this sequence version replaced g1:6970517.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE Center: Whitehead Institute/ MIT Center for Genome Research

JOURNAL Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu

COMMENT ----- Project Information
 Center project name: I4345
 Center clone name: 69-A_7
 ----- Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 166563 bases at least Q40
 Consensus quality: 165997 bases at least Q30
 Consensus quality: 174469 bases at least Q20
 Insert size: 181000; agarose-fp
 Insert size: 173280; sum of contigs
 Quality coverage: 5.2 in Q20 bases; agarose-fp
 Quality coverage: 5.4 in Q20 bases; sum-of-contigs

----- * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 * 378 477: contig of 377 bp in length
 * 478 1740: gap of 100 bp
 * 1741 1840: contig of 1263 bp in length
 * 1841 401: contig of 2191 bp in length
 * 4032 4131: gap of 100 bp
 * 4132 999: contig of 5838 bp in length
 * 9970 10069: gap of 100 bp
 * 10070 17346: contig of 7277 bp in length
 * 17347 17446: gap of 100 bp
 * 17447 29159: contig of 11713 bp in length
 * 29160 29259: gap of 100 bp
 * 29260 44992: contig of 15733 bp in length

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* 44993 45092; gap of 100 bp
* 45093 63565; contig of 18473 bp in length
* 63566 63665; gap of 100 bp
* 63666 82201; contig of 18536 bp in length
* 82202 82302; gap of 100 bp
* 82302 105742; contig of 23441 bp in length
* 105743 105842; gap of 100 bp
* 105843 139307; contig of 33465 bp in length
* 139308 139408; gap of 100 bp
* 139408 174380; contig of 34373 bp in length.

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                /note="assembly_fragment"
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                g 53658 t 1103 others

BASE COUNT        ORIGIN
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ORIGIN
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Best Local Similarity 63..4%; Pred. No. 0 0096; 37; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY   52 GAGATCCAAAGTGCAGAAGGAGAAATGGTGGAGGCTATTATCCCCAGTGCCCTTCCTG 111
Db 154021 GAGATGGGAGAGAAATAGCAAGTCATGATATTGTTCCCTGTAGCTACATCCATG 154080

QY   112 CTGGGTATGGATGAACAGTGGCTGACTTCATGGAAAG 152
Db 154081 CAGGGCCACTGGTGGCAGTGTCTCTAGTAAAG 154121

RESULT 11
AC112498/C LOCUS          Homo sapiens X BAC RP11-639A7 bp DNA linear
DEFINITION    Homo sapiens X BAC RP11-639A7 (Roswell Park Cancer Institute Human
AC112498          BAC Library) complete sequence.
ACCESSION    AC112498..3 GI:21591809
KEYWORDS    HTG.
SOURCE      human
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butherida; Primates; Catarrhini; Hominidae; Homo;
REFERENCE  1 (bases 1 to 175559)

```

| AUTHORS | ADDITIONAL INFORMATION |
|---|------------------------|
| Muzny, D.M., Adams, C., Adjo-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S. L., Amaraltinge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimaha, K., Blanckenhagen, K., Bonnian, D., Bouck, J., Bowles, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buñuel, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Cox, R., Chen, Z., Chowdry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Datphorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delgadillo, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, D., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhanj, C., Escoto, M., Falis, F., Ferragut, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guerava, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hayes, A., Hernandez, J., Hernandez, Q., Hodgeson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, R., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvay, J., Kovari, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, Z., Lichartage, O., Lieu, C., Liu, J., Liu, W., Louisedge, H., Lozano, R.J., Lu, X., Lucier, R., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, B., Massey, E., Mawhinney, R., McLeod, M.P., Medior, M., Meij, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newson, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokekwu, S., Ogwu, M., Okwounou, G., Oraquigne, N., Okivedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ran, Y., Rives, M., Rojas, A., Rojano, J.I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatley, C.A., Tabor, T., Tamersisa, A., Thomas, N., Tang, H., Tansey, J., Taylor, C., Taylor, H., Taylor, T., Telefrod, B., Thomas, S., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Washington, S., Williams, G., Williams, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, J., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D. | |

| | | |
|---------------|-----------------|--|
| Worley, K. C. | JOURNAL ARTICLE | Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA |
| Worley, K. C. | JOURNAL ARTICLE | Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA |
| Worley, K. C. | JOURNAL ARTICLE | Submitted (14-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA |
| Worley, K. C. | JOURNAL ARTICLE | Submitted (26-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA |

REFERENCE 5 (bases 1 to 175559)
AUTHOR Worley, K.C.
JOURNAL Direct Submission
TITLE Submitted (28-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Jun 26, 2002 this sequence version replaced gi:20335921.
INFORMATION http://www.hgsc.bcm.tmc.edu or email gc-help@bcm.tmc.edu

CLOSE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are on sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.

Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
 SRSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
 Repeats are identified using RepeatMasker (A. Smit and P. Green unpublished.) for Human and Mouse sequences.
 Genes and Region of sequence similarity are identified by BLAST (NUC. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.edu:8088/quality.info/gnb.html>.

Location/Qualifiers
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/chromosome="X"
/clone="RP11-699A7"
1. .2494
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1. .2004
/note="overlaps bases 123282..125285 of clone AC121340."
_region
feature

Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., Dearlton,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardya,S.,
 Ginde,S., Gord,S., Goyette,L., Graham,L., Grand-Pierre,N.,
 Hages,B., Horton,L., Huile,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lanazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
 Macdonald,D.P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 McEvany,P., McFarland,K., Meldrim,J., Maneus,L., Mihova,T.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Piere,N., Pollara,V., Raymond,C.,
 Retta,R., Relebach,M., Riley,R., Rize,P., Ronan,J.,
 Rosetti,M., Roy,A., Santos,R.R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talama,J., Testore,J., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 13, 2002 this sequence version replaced g1:18308592.
 All repeats were identified using RepeatMasker:
 Smit,A.F.A. & Green,P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www.seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L22007
 Center Clone name: 640_C_18

* * * * * NOTE: This record contains 73 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

| |
|--|
| * * * * * 1. 679: contig of 679 bp in length * * * * * 680 779: gap of 100 bp * * * * * 780 1492: contig of 713 bp in length * * * * * 1493 1592: gap of 100 bp * * * * * 1593 2305: contig of 713 bp in length * * * * * 2306 2405: gap of 100 bp * * * * * 2406 3042: contig of 637 bp in length * * * * * 3043 3142: gap of 100 bp * * * * * 3143 3855: contig of 713 bp in length * * * * * 3856 3955: gap of 100 bp * * * * * 3956 4648: contig of 693 bp in length * * * * * 7057 7156: gap of 100 bp * * * * * 4649 4748: gap of 100 bp * * * * * 4749 5465: contig of 717 bp in length * * * * * 5466 5565: gap of 100 bp * * * * * 5566 6259: contig of 694 bp in length * * * * * 6260 6359: gap of 100 bp * * * * * 6356 7056: contig of 697 bp in length * * * * * 7157 7810: gap of 100 bp * * * * * 7811 7910: contig of 654 bp in length * * * * * 7911 8627: contig of 717 bp in length * * * * * 8628 8727: gap of 100 bp * * * * * 8728 940: contig of 673 bp in length * * * * * 9401 9500: gap of 100 bp * * * * * 10215 10314: contig of 714 bp in length * * * * * 10315 10316: gap of 100 bp |
|--|

| | | | |
|-------|---------|------------------|-----------|
| 10315 | 11020: | contig of 706 bp | in length |
| 11121 | 11120: | gap of 100 bp | |
| 11121 | 111846: | contig of 726 bp | in length |
| 11847 | 11946: | gap of 100 bp | |
| 11947 | 12661: | contig of 715 bp | in length |
| 12662 | 12751: | gap of 100 bp | |
| 12751 | 13467: | contig of 706 bp | in length |
| 13468 | 13592: | gap of 100 bp | |
| 13593 | 14270: | contig of 704 bp | in length |
| 14272 | 14371: | gap of 100 bp | |
| 14372 | 15069: | contig of 698 bp | in length |
| 15070 | 15159: | gap of 100 bp | |
| 15170 | 15882: | contig of 713 bp | in length |
| 15893 | 15982: | gap of 100 bp | |
| 15983 | 16700: | contig of 718 bp | in length |
| 16701 | 16800: | gap of 100 bp | |
| 16801 | 17501: | contig of 701 bp | in length |
| 17502 | 17601: | gap of 100 bp | |
| 17602 | 18328: | contig of 727 bp | in length |
| 18329 | 18438: | gap of 100 bp | |
| 18429 | 19117: | contig of 689 bp | in length |
| 19118 | 19217: | gap of 100 bp | |
| 19218 | 19925: | contig of 708 bp | in length |
| 19926 | 20052: | gap of 100 bp | |
| 20026 | 20755: | contig of 730 bp | in length |
| 20756 | 20855: | gap of 100 bp | |
| 20856 | 21556: | contig of 711 bp | in length |
| 21567 | 21666: | gap of 100 bp | |
| 21667 | 22374: | contig of 708 bp | in length |
| 22375 | 22414: | gap of 100 bp | |
| 22475 | 23181: | contig of 707 bp | in length |
| 23182 | 23281: | gap of 100 bp | |
| 23282 | 24001: | contig of 720 bp | in length |
| 24002 | 24101: | gap of 100 bp | |
| 24102 | 24811: | contig of 710 bp | in length |
| 24812 | 24911: | gap of 100 bp | |
| 24912 | 25600: | contig of 689 bp | in length |
| 25601 | 25700: | gap of 100 bp | |
| 25701 | 26422: | contig of 722 bp | in length |
| 26423 | 26522: | gap of 100 bp | |
| 26523 | 27228: | contig of 706 bp | in length |
| 27229 | 27328: | gap of 100 bp | |
| 27329 | 28041: | contig of 713 bp | in length |
| 28042 | 28141: | gap of 100 bp | |
| 28142 | 28844: | contig of 703 bp | in length |
| 28845 | 28948: | gap of 100 bp | |
| 28945 | 29628: | contig of 684 bp | in length |
| 29629 | 29728: | gap of 100 bp | |
| 29729 | 30423: | contig of 695 bp | in length |
| 30242 | 30523: | gap of 100 bp | |
| 30524 | 31235: | contig of 712 bp | in length |
| 31236 | 31335: | gap of 100 bp | |
| 31336 | 31919: | contig of 644 bp | in length |
| 31980 | 32079: | gap of 100 bp | |
| 32079 | 32797: | contig of 718 bp | in length |
| 32798 | 32897: | gap of 100 bp | |
| 32898 | 33595: | contig of 698 bp | in length |
| 33596 | 33695: | gap of 100 bp | |
| 33696 | 34416: | contig of 721 bp | in length |
| 34417 | 34516: | gap of 100 bp | |
| 34517 | 35335: | contig of 719 bp | in length |
| 35236 | 35335: | gap of 100 bp | |
| 35336 | 36034: | contig of 699 bp | in length |
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| 36135 | 36646: | contig of 712 bp | in length |
| 36647 | 36948: | gap of 100 bp | |
| 36947 | 37670: | contig of 724 bp | in length |
| 37671 | 37770: | gap of 100 bp | |
| 37771 | 38479: | contig of 709 bp | in length |
| 38480 | 38579: | gap of 100 bp | |
| 38580 | 39987: | contig of 708 bp | in length |
| 39388 | 40105: | contig of 718 bp | in length |

Query Match 22.7%; Score 41.6; DB 2; Length 58693;
 Best Local Similarity 62.5%; Pred. No. 0.011; Indels 0; Gaps 0;
 Matches 65; Conservative 0; Mismatches 39;

| | | |
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| Db | 38355 | AGGGCAGGGAGAGTCAGGTCTCACTTCTCTGCTACCCCTATGTGCC 38414 |
| Qy | 119 | ATGGATGAAAGTAGGGCTGACTTCATCTAGGAAAGGCTATGGCT 162 |
| Db | 38415 | ATGATTATAGTGCTTCTCACCAAGGATAGCTC 38458 |

RESULT 14
 AP005368/C LOCUS 111461 bp DNA linear PRI 30-JUL-2002
 DEFINITION Homo sapiens genomic DNA, chromosome 8q23, clone: KB870F5, complete
 SOURCE AP005368_2 GI:22004069
 VERSION AP005368
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 ORGANISM Homo sapiens pre-pro-B cell cell-line:FLEB 14 - 14 DNA,
 Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
 Mammalia; Eutheria; Primates;
 Shimizu, N. and Asakawa, S.
 Homo sapiens DNA chromosome 8 SEQUENCE
 clone_1b:Keio BAC library clone:KB870F5.

REFERENCE 1
 AUTHORS Shimizu, N. and Asakawa, S.
 TITLE Homo sapiens DNA chromosome 8 SEQUENCE
 JOURNAL Published Only in Database (2002)
 2 (bases 1 to 111461)
 AUTHORS Shimizu, N. and Asakawa, S.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-2002) Nobuyoshi Shimizu, Keio University, School
 of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo

160-8582, Japan (E-mail:inshimizudbm.med.keio.ac.jp,
 Tel:81-3-3351-2370, Fax:81-3-3351-2370)
 On Jul 30, 2002 this sequence version replaced gi:21280421.
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 /clone_lib="Keio BAC library"
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 5369..5399
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Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L21920
 Center clone name: 91_D_24

 FEATURES Source

 Location/Qualifiers
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 TITLE JOURNAL

 Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 149126)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., repeat_region
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., repeat_region
 Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., repeat_region
 Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., repeat_region
 Cook,A., Cooke,P., DeArellano,K., Diaz,J.S., Dodge,S., repeat_region
 Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagyna,S., repeat_region
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., repeat_region
 Hagos,B., Horton,L., Iliev,I., Hulme,W., Jones,C., repeat_region
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., repeat_region
 Landers,T., Lehozky,J., Levine,R., Lindblad-Toh,K., Liu,G., repeat_region
 MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,L., repeat_region
 Mihrava,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., repeat_region
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., repeat_region
 Oliver,J., Peterson,K., Phunkhang,P., Roy,A., Schauer,S., Schupback,R., repeat_region
 Roman,J., Rosetti,M., Santos,R., Strange-Thomann,N., Stojanovic,N., repeat_region
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 Strauss,N., Subramanian,A., Talamas,J., Trigilio,J., Vassiliev,H., repeat_region
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., repeat_region
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., repeat_region
 Zainoun,J., Zembok,L., Zimmer,A., and Zody,M.
 Direct Submission

 Submitted (29-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 149126)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., repeat_region
 Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., repeat_region
 Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., repeat_region
 Cook,A., Cooke,P., DeArellano,K., Diaz,J.S., Dodge,S., repeat_region
 Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagyna,S., repeat_region
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 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., repeat_region
 Zainoun,J., Zembok,L., Zimmer,A., and Zody,M.
 Direct Submission

 Submitted (01-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 29, 2002 this sequence version replaced g1:20334653.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center

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